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| RX-MEDLINE=95300228; PubMed=870664; | RA-Bouhaouala-Zahar H., RA-Ducane P., RA-Zenouaki I., RA-Ben Khalifa R., RA-Pehrke M., RA-Boulain J.C., RA-el Ayeb M., RA-Menez A., RA-Karoui H.; |
| PT-Clustacean-specific toxin 1; | RT-"A recombinant insect-specific alpha-toxin of <i>Buthus occitanus tunetanus</i> confers protection against homologous mammal toxins."; |
| PT-Eukaryota; Metazoa; Arthropoda; Chelicera; Arachnida; Scorpiones; | RT- <i>Buthus</i> ; Biochem. 238:653-660(1996). |
| NCBI-TaxID=29941; | CC--FUNCTION: Binds to sodium channels and inhibits the inactivation of the activated channels, thereby blocking neuronal transmission. |
| CC-SEQUENCE: DISULFIDE BONDS, AND STRUCTURE BY NMR. | CC--SUBCELLULAR LOCATION: Secreted. |
| CC-MEDLINE=95244424; PubMed=7727165; | CC--TISSUE/SPECIFICITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| Lebreton F., Delpech M., Ramirez A.R., Baldewitz C., Possani L.D.; | CC--SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| Lebreton F., Delpech M., Ramirez A.R., Baldewitz C., Possani L.D.; | CC--This toxin is active only on insects. |
| Clustacean toxin from the venom of the scorpion <i>Centruroides limpidus limpidus</i> Karsch."; | CC--SUBCELLULAR LOCATION: Subcellular. |
| Chemistry 33:1135-1149(1994); | CC--This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). |
| CC-FUNCTION: Binds to sodium channels and inhibits the inactivation of the activated channels, thereby blocking neuronal transmission. | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| CC-SUBCELLULAR LOCATION: Secreted. | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| CC-TISSUE/SPECIFICITY: Expressed by the venom gland. | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| CC-SIMILARITY: Beta-toxin subfamily. | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| CC-PIR: A55892; A55869; | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| CC-HSSP: F01492; VYNB; | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| CC-InterPro: IPR01614; Knot1; | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| CC-InterPro: IPR02119; Neurotoxin; | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| CC-InterPro: IPR02361; Scorpion_toxin_nl; | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| CC-InterPro: IPR0437; toxin_3_1; | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| CC-PIRINTS: PRG3284; TOXIN; | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| CC-FUNCTION: SCOPC038; Scorpion_toxin_1; | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| CC-SMART: SW00535; Knot1_1; | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| CC-Toxin: Neurotoxin; Iont;_1; | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| CC-DISULFID 12 65 | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| CC-DISULFID 16 41 | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| CC-DISULFID 25 46 | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| CC-DISULFID 29 41 | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| CC-SEQUENCE 66 AA; | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| Alignment Scores: | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| Score: 0.0:51 | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| Core: 79.50 | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| Percent Similarity: 53.85% | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| Best Local Similarity: 43.59% | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| Query Match: 29.78% | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| DB: 13 | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| Result 7: | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| SCX4_BUTOC STANDARD; PRT: 85 AA. | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| SCX4_BUTOC STANDARD; PRT: 65 AA. | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| QI:7254; | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| DT-15-DEC-1998 (Rel. 37. Created) | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| DT-15-DEC-1998 (Rel. 37. Last sequence update) | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| DT-28-FEB-2003 (Rel. 41. Last annotation update) | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| DE-Neurotoxin XIV precursor (Bot14); | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| DE-Buthus occitanus tunetanus (Common European scorpion); | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| DC-Buthuryota; Metazoa; Arthropoda; Chelicera; Arachnida; Scorpiones; | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| DC-Buthuryota; Buthidae; Buthus. | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| NCBI-TaxID=6871; | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| RN-SEQUENCE FROM N.A. | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| RP-TCSSL Version | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| RN-NCB_TaxID=6869; | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| RN- | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| Result 8: | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| SCX4_BUTOC STANDARD; PRT: 85 AA. | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| SCX4_BUTOC STANDARD; PRT: 65 AA. | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| AC-P9354; | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| DT-28-FEB-2003 (Rel. 41. Created) | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| DT-28-FEB-2003 (Rel. 41. Last sequence update) | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| DT-15-SEP-2003 (Rel. 42. Last annotation update) | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| DE-Alpha-like neurotoxin IV (Bot4); | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| OS-Buthus occitanus mardohei (Moroccan scorpion); | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| OC-Buthuryota; Metazoa; Arthropoda; Chelicera; Arachnida; Scorpiones; | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| OC-Buthidae; Buthidae; Buthus. | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| NCB_TaxID=6869; | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| RN- | CC--SEQUENCE: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. |

SEQUENCE, PHARMACOLOGICAL CHARACTERIZATION, AND MASS SPECTROMETRY.

TISSUE-Venom; PubMed=10103091;

MEDLINE=99203324; PubMed=2279844;

RN Cestele S., Stankiewicz P., De Waard M., Dargent B.,

Gilles N., Rochat H., Martin-Bauchaire M.-F., Gordon D.,

"Scorpion alpha-like toxins, toxic to both mammals and insects, differentially interact with receptor site 3 on voltage-gated sodium channels in mammals and insects."

Bur. J. Neurosci. 11:975-985(1999).

-!- FUNCTION: Binds to sodium channels and inhibits the inactivation of the activated channels, thereby blocking neuronal transmission.

-!- SUBCELLULAR LOCATION: Secreted.

-!- TISSUE SPECIFICITY: Expressed by the venom gland.

-!- MASS SPECTROMETRY: MW=1287.96; MW ERA=0.37; METHOD=Electrospray.

-!- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.

CC ALPHA-TOXIN SUBFAMILY: ALPHA-LIKE TOXIN SUBCLASS.

Pfam: PF0057; toxin_3; 1.

ProDom: PD000908; Scorpion_toxinL; 1.

DR SMART: SM0305; Knot1; 1.

Toxin: Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor.

DISULFID 12 63 BY SIMILARITY.

DISULFID 16 36 BY SIMILARITY.

DISULFID 22 46 BY SIMILARITY.

DISULFID 26 48 BY SIMILARITY.

SEQUENCE 65 AA: 4305EB32436AAB90 CRC64;

Alignment Scores:

Dy 16 TCTTCGTTGGGTGCTGTGAACCTACACTTGGATGCCAACCGTGAGTCAGGAGG 75

: : : : : | :

Db 11 AsnCysValTyrglycysAlaLys--AsnSerTyrcysAsnAspLeuCysThrLysAsn 29

Percent Similarity: 51.22%

Best Local Similarity: 39.02%

Query Match: 29.40%

DB: 1

Gaps: 3

RN

US-09-673-274B-2_COPY_1_132 (1-132) × SCX4_BUTOM (1-65)

Alignment Scores:

Dy 11 AsnCysValTyrglycysAlaLys--AsnSerTyrcysAsnAspLeuCysThrLysAsn 29

Percent Similarity: 51.22%

Best Local Similarity: 39.02%

Query Match: 29.40%

DB: 1

Gaps: 3

RN

Dy 127 GAG 129

Db 49 Glu 49

RN

STANDARD; PRT; 84 AA.

RN

SCX3_ANDAU

P0460; 21-JUL-1986 (Rel. 01, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Neurotoxin III Precursor (AAH3).)

DS Androctonus australis hector (Sahara scorpion)

Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;

Buthidae; Buthidae; Androctonus; NCBI TaxID=70175;

OX [1]

RN SEQUENCE FROM N.A.

RX MEDLINE=00037062; PubMed=2808423;

Qy Bougi P.E., Rochat H., Smith L.A.;

DB "Precursors of Androctonus australis scorpion neurotoxins. Structures

of precursors, processing outcomes, and expression of a functional

recombinant toxin II." J. Biol. Chem. 26:19259-19265 (1989).

RN SEQUENCE OP 20-83.

RX MEDLINE=1914814; PubMed=428402;

RA Koeyan C., Martinez G., Rochat H.;

"Amino acid sequence of neurotoxin III of the scorpion Androctonus

RN austrialis Hector." Eur. J. Biochem. 94:609-615 (1979).

RN [3]

RN STRUCTURE BY NMR; PubMed=2279844;

RX MEDLINE=91122921; PubMed=2279844;

RA Laplante S.R., Mikou A., Roblin M., Guillet E., Delusuc M.A.,

RA Charpentier J., Lallemand J.-Y.

RT "Rapid determination and NMR assignments of antiparallel sheets and

helices of a scorpion and a cobra toxin." Int. J. Pept. Protein Res. 36:227-230 (1990).

RN [4]

RN STRUCTURE BY NMR; PubMed=91044377; PubMed=1422146;

RA Mikou A., Laplante S.R., Guillet E., Lallemand J.-Y., Martin-Eauclaire M.-F., Rochat H.;

RT "Toxin III of the scorpion Androctonus australis hector: proton nuclear magnetic resonance assignments and secondary structure." J. Biomol. NMR 2:57-70 (1992).

RN FUNCTION: Binds to sodium channels and inhibits the inactivation of the activated channels, thereby blocking neuronal transmission.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.

CC -!- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.

CC -!- ALPHA-TOXIN SUBFAMILY: Alpha-Toxin Subfamily.

CC -!- SUBCELLULAR LOCATION: Secreted.

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CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.

| | | |
|---|--|--|
| ID: AC: | SC46 LEIGH: STANDARD; PRT; 64 AA. | RA: Kopeyan C., Martinez G., Rochat H.; "Primary structure of toxin IV of <i>Leiurus quinquestriatus</i> " |
| DT: 28-FEB-2003 [Rel. 4]; Last sequence update; | RT: RFL: 181:211-217 (1985). | RT: "FUNCTION: Bands to sodium channels and inhibits the inactivation of the activated channels, thereby blocking neuronal transmission. |
| DT: 15-SEP-2003 [Rel. 42]; Last annotation update; | CC: -!- SUBCELLULAR LOCATION: Secreted. | CC: -!- TISSUE SPECIFICITY: Expressed by the venom gland. |
| DE: Alpha-like neurotoxin Lqh VI (Lqh6); | CC: -!- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. | CC: -!- ALPHA-BETA-TOXIN SUBFAMILY. |
| CS: <i>Leiurus quinquestriatus</i> hebreus (Yellow scorpion); | DR: PIR: Ad1749; NTSM4L; HSSP: D45697; ISNL; InterPro: IPR00314; Knot1; InterPro: IPR00119; Neurotoxin; InterPro: IPR0261; Scorpion_toxin1. | DR: PIR: Ad1749; NTSM4L; HSSP: D45697; ISNL; InterPro: IPR00314; Knot1; InterPro: IPR00119; Neurotoxin; InterPro: IPR0261; Scorpion_toxin1. |
| OC: Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones; | DR: PF00537; toxin 3; 1. PRINTS: PR00284; TCXIN; PRODOM: PDC00908; Scorpion_toxin1; 1. | DR: PF00537; toxin 3; 1. PRINTS: PR00284; TCXIN; PRODOM: PDC00908; Scorpion_toxin1; 1. |
| OC: Arthropoda; Butidae; <i>Leiurus</i> . | DR: SMART: SMOG05; Knot1; 1. Toxin: Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor; Amidation. | DR: SMART: SMOG05; Knot1; 1. Toxin: Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor; Amidation. |
| DN: NCBI_TaxID=6884; | DR: FT: DISULFID 13 64 BY SIMILARITY. FT: DISULFID 17 37 BY SIMILARITY. FT: DISULFID 23 47 BY SIMILARITY. FT: DISULFID 27 49 BY SIMILARITY. FT: MOD RES 65 65 AMIDATION. | DR: FT: DISULFID 13 64 BY SIMILARITY. FT: DISULFID 17 37 BY SIMILARITY. FT: DISULFID 23 47 BY SIMILARITY. FT: DISULFID 27 49 BY SIMILARITY. FT: MOD RES 65 65 AMIDATION. |
| RN: SEQUENCE, PHARMACOLOGICAL CHARACTERIZATION, AND BIOASSAY. | SQ: SEQUENCE 65 AA: 7202 MW; B82102EC1C2BB9F6 CRC64; | Alignment Scores: Pred. No.: 0.0276 Length: 65 Score: 77.50 Matches: 16 Percent Similarity: 57.14% Conservative: 8 Best Local Similarity: 38.10% Mismatches: 9 Query Match: 29.03% Indels: 9 DB: 12 AsnysvaVtyrhrcyglyserAsnserYr-----CysAenthrglycylcysthr 28 |
| RC: TISSUE: Venom; | US-09-673-274B-2_COPY_1_132 (1-132) × SCX4_LEIQU (1-65) | US-09-673-274B-2_COPY_1_132 (1-132) × SCX4_LEIQU (1-65) |
| RA: MEDLINE=22168981; PubMed=12180969; | QY: 16 TCCTRGGCTGTGG-----GGTGGCTGTGAACTACACTTCGATGCCAGGGTAGTGCAAG 69 | QY: 16 TCCTRGGCTGTGG-----GGTGGCTGTGAACTACACTTCGATGCCAGGGTAGTGCAAG 69 |
| RA: Hamon A., Gilles N., Sauvage P., Martineau A., Kopeyan C., Jlens C., Tytgat G., Lancelin J.-M., Gordon D.; "Characterization of scorpion alpha-like toxin group using two new toxins from the scorpion <i>Leiurus quinquestriatus hebraeus</i> "; Eur. J. Biochem. 269:3920-3933(2002). | DB: 12 AsnysvaVtyrhrcyglyserAsnserYr-----CysAenthrglycylcysthr 28 | DB: 12 AsnysvaVtyrhrcyglyserAsnserYr-----CysAenthrglycylcysthr 28 |
| RA: -!- SUBCELLULAR LOCATION: Secreted. | QY: 70 AGGGGGTTTCAAGGGTGTCACTGC-----GGTTGCTTCTGCTAACGTGAAGTC 120 | QY: 70 AGGGGGTTTCAAGGGTGTCACTGC-----GGTTGCTTCTGCTAACGTGAAGTC 120 |
| RA: !- TISSUE/SPECIFICITY: Expressed by the venom gland. | DB: 29 LysasnGlyAlaGluSerGlytyrCysClnTrpLeuGlyLysYrglyAsnAla---Cys 47 | DB: 29 LysasnGlyAlaGluSerGlytyrCysClnTrpLeuGlyLysYrglyAsnAla---Cys 47 |
| RA: !- XISCIERANEUCOS: LD(50) is 34.3 nmol/kg to cockroaches (<i>Blattella germanica</i>). | QY: 121 TGGTGC 126 | QY: 121 TGGTGC 126 |
| RA: !- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. | DB: 48 TrpCys 49 | DB: 48 TrpCys 49 |
| RA: ALPHA-BETA-TOXIN SUBFAMILY, ALPHA-LIKE TOXIN SUBCLASS. | RESULT 12 | RESULT 12 |
| RA: PFM: PF00537; toxin 3; 1. | SCAT_MESMA ID: SCAT_MESMA STANDARD; PRT; 85 AA. | SCAT_MESMA ID: SCAT_MESMA STANDARD; PRT; 85 AA. |
| RA: PRODOM: PDC00908; Scorpion_toxin1; 1. | AC: Q9UAC8; 27 | AC: Q9UAC8; 27 |
| RA: SWRT: SM00505; Knot1; 1. | DT: 28-FEB-2003 (Rel. 41, Created) | DT: 28-FEB-2003 (Rel. 41, Last sequence update) |
| RA: Toxin: Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor; Amidation. | DT: 28-FEB-2003 (Rel. 41, Last annotation update) | DT: 28-FEB-2003 (Rel. 41, Last annotation update) |
| RA: DISTFIELD: 12 62 BY SIMILARITY. | DE: Neurotoxin AS-1 precursor. | DE: Neurotoxin AS-1 precursor. |
| RA: DISULFID: 16 34 BY SIMILARITY. | OS: <i>Mesobuthus martensii</i> (Manchurian scorpion) (Butchus martensis). | OS: <i>Mesobuthus martensii</i> (Manchurian scorpion) (Butchus martensis). |
| RA: DISULFID: 20 44 BY SIMILARITY. | OC: Bukaryota; Metazoa; Archropoda; Cheicerata; Arachnida; Scorpiones; OC: Butioidae; Butidae; Mesobuthus. | OC: Butioidae; Butidae; Mesobuthus. |
| RA: DISULFID: 24 46 BY SIMILARITY. | RN: NCBI_TaxID=34649; | RN: NCBI_TaxID=34649; |
| RA: MCJ RES: 64 64 AMIDATION. | RC: SEQUENCE FROM N.A. | RC: SEQUENCE FROM N.A. |
| RA: SEQUENCE 64 AA: 6603 MW; 49A54B0B6C75392E CRC64; | RA: Lan Z.-D., Dai L., Chi C.-W.; "The gene cloning and sequencing of AS and AS-1, two novel neurotoxins from the scorpion <i>Butchus martensi</i> Karisch"; Submitted (AUG-1998) to the EMBL/Genbank/DBJ databases. | RA: Lan Z.-D., Dai L., Chi C.-W.; "The gene cloning and sequencing of AS and AS-1, two novel neurotoxins from the scorpion <i>Butchus martensi</i> Karisch"; Submitted (AUG-1998) to the EMBL/Genbank/DBJ databases. |
| RA: Alignment Scores: Pred. No.: 0.0276 Length: 64 Score: 77.50 Matches: 15 Percent Similarity: 51.28% Conservative: 5 Best Local Similarity: 38.46% Mismatches: 5 Query Match: 29.03% Indels: 2 DB: 28 | QY: 28 GlyGlyThrGlyHisCysGlyPhylsLysGlyIleAlaCysTrpCys 46 | QY: 28 GlyGlyThrGlyHisCysGlyPhylsLysGlyIleAlaCysTrpCys 46 |
| RA: PRT: 64 AA. | RESULT 11 | RESULT 11 |
| RA: DT: 2-JUL-1986 (Rel. 01, Created) | SCX4_LEIQU ID: SCX4_LEIQU STANDARD; PRT; 65 AA. | SCX4_LEIQU ID: SCX4_LEIQU STANDARD; PRT; 65 AA. |
| RA: DT: 28-FEB-2003 (Rel. 41, Last sequence update) | AC: P01489; 27 | AC: P01489; 27 |
| RA: DE: Neurotoxin IV (Lqh IV) (Lqh4) | DT: 28-FEB-2003 (Rel. 41, Last annotation update) | DT: 28-FEB-2003 (Rel. 41, Last annotation update) |
| RA: OS: <i>Leiurus quinquestriatus</i> (Egyptian scorpion); | DE: Neurotoxin IV (Lqh IV) (Lqh4) | DE: Neurotoxin IV (Lqh IV) (Lqh4) |
| RA: UC: Eukaryota; Metazoa; Archropoda; Chelicerata; Arachnida; Scorpiones; UC: Butioidae; Butidae; <i>Leiurus</i> . | CC: -!- FUNCTION: Ryanodine receptor agonist in skeletal muscle. | CC: -!- FUNCTION: Ryanodine receptor agonist in skeletal muscle. |
| RA: CX: NCB-TaxID=6885; | CC: -!- SUBCELLULAR LOCATION: Secreted (By similarity). | CC: -!- SUBCELLULAR LOCATION: Secreted (By similarity). |
| RA: RN: - | CC: -!- TISSUE SPECIFICITY: Expressed by the venom gland. | CC: -!- TISSUE SPECIFICITY: Expressed by the venom gland. |
| RA: SEQUENCE | | |

ALPHA-TOXIN SUBFAMILY.

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EMBL: AF079061; AAD47375.1; -.
HSSP: P01492; 1VNB.
InterPro: IPR03614; Knot1.
DR InterPro; IPR002061; Scorpion_toxinL.
PFAM: PF00532; toxin_3; 1.
DR PFAM; PD00908; Scorpion_toxinL; 1.
SMART: SM00505; Knot1; 1.
Toxin: Neurotoxin; Signal.

POTENTIAL.
CHAIN 19
CHAIN 20
NEUROTOXIN AS-1.
PT DISULFID 31 BY SIMILARITY.
PT DISULFID 35 BY SIMILARITY.
PT DISULFID 42 BY SIMILARITY.
PT DISULFID 46 BY SIMILARITY.
SEQUENCE 85 AA; 9802 MW; E2274838439E2B95 CRC64;

Alignment Scores:
Score: 0.0327
Percent Similarity: 53.49%
Best Local Similarity: 39.53%
Query Match: 28.44%
DB: JS-09-673-274B-2_COPY_1_132 (1-132) x SCAT_MESNA (1-85);

Qy 1 GATNAGCTTATCGGTTCTGCGTGTGGGTGAACTACATTGGATGAAACGGT 60
26 AsnIysTyrThrGlyCysIysIleTrpysValleAsnGluSe:-:--CysAsnSer 44
Dy 61 GAGGCCAAGGAGCGGTTACAGGGTGGTCACTGGCTTCCCTCGTAACGTGAACTGC 120
45 GlucysLysLeuIysArgGlyAsnTyrglyTyryrFys---TyrPheTrpLysLeuAlaCys 63
Dy 121 TCGTGCAG 129
Db 64 TyrcysGlu 66

RESULT 13

SIXX2-LEIQU

STANDARD; PRT; 61 AA.

AC P19855; 01-FEB-1991 (Rel. 17, Created)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DS Insect toxin 2 (Insect toxin LgG1T2).
DS Leurus quinquestriatus (Egyptian scorpion).
DS Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
DC Buthoidea; Butchidae; Leirus.
DX NCBI_TaxID=6885; [1]

SEQUENCE
MEDLINE=9018494; PubMed=2311768;
Kopeyan C., Mansuelle P., Sampieri F., Brando T., Bahraoui E. M.,
Rochat H., Granier C.;
"Primary structure of scorpion anti-insect toxins isolated from the venom of Leirus quinquestriatus quinquestriatus.";
FEBS Lett. 261:423-426(1990).

SEQUENCE
MEDLINE=3166530; PubMed=8431601;
Zlotkin E., Gurevitz M., Fowler E., Adams M.E.;
"Depressant insect selective neurotoxins from scorpion venom:

CC Chemistry, action, and gene cloning.";
RN [3] Arch. Insect Biochem. Physiol. 22:55-73(1993).

CC ACTION.
RN P0982; 01-MAR-1989 (Rel. 10, Created)
RA On the chemistry and action of the depressant insect toxins.";

CC RT Toxinon 28:170-17C(1990)
RL FUNCTION: Binds to sodium channels and inhibits the inactivation of the activated channels, thereby blocking neuronal transmission.

CC This toxin induces a slow, depressive, flaccid paralysis on fly larvae. It is active only on insects.

CC SUBCELLULAR LOCATION: Secreted.

CC TISSUE SPECIFICITY: Expressed by the venom gland.

CC SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.

CC ALPHA-TOXIN SUBFAMILY.

CC HSSP: P01394; 2SN3.

CC InterPro: IPR00314; Knot1.

CC SMART: SM00505; Knot1; 1.

CC Toxin: Neurotoxin; Ionic channel_inhibitor; Sodium channel_inhibitor.

CC KW By SIMILARITY.

CC FT DISULFID 10 60

CC FT DISULFID 14 35

CC FT DISULFID 21 42

CC FT DISULFID 25 44

CC SQ SEQUENCE 61 AA; 6860 MW; 8CF01771C7DCFAF6 CRC64; 2

CC Alignment Scores:
Pred. No.: 0.0327 Length: 61
Score: 77.40 Matches: 76.50
Percent Similarity: 53.49% Conservativeness: 61
Best Local Similarity: 39.53% Mismatches: 15
Query Match: 28.44% Indels: 5
DB: 1 Gaps: 2

CC Score: 76.50 Length: 61
Percent Similarity: 55.26% Matches: 15
Best Local Similarity: 39.47% Conservative: 6
Query Match: 28.65% Mismatches: 5
DB: 1

CC DB: 1 Gaps: 2

CC US-09-673-274B-2_COPY_1_132 (1-132) x SIXX2-LEIQU (1-61);

CC Qy 16 TCCCTGGTGGGGGTTCTGTAACTACACTCCGATTGGCAACGGTGAGTGTGGAGGAGGAGG;
CC Db 13 SerCysLeuPheGly -----AsnGluGlyCysasnLysGluCysLysserTyr 26

CC OS Neurotoxin M14.

CC DQ Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;

CC OC Buthoidea; Butchidae; Mesobuthus.

CC OX NCBITaxID=34648; 1

CC RN 11] 1
CC SEQUENCE
RC TISSUE=venom; MEDLINE=8046632; PubMed=6497916;
RX RA Volkova T.M., Garsia A.F., Telezhinskaya I.N., Potapenk N.A.,
RA Grishin E.V.;
RT "Amino acid sequence of 2 neurotoxins from the scorpion Buthus eupeus venom.";
RL Bicorg, Khim. 10:979-982(1984).
CC CC FUNCTION: Binds to sodium channels and inhibits the inactivation of the activated channels, thereby blocking neuronal transmission.
CC CC Has paralytic activity in mice.
CC CC SUBCELLULAR LOCATION: Secreted.
CC CC TISSUE SPECIFICITY: Expressed by the venom gland.

CC -- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.

CC ALPHA_TOXIN SUBFAMILY.

CC PIR: JTO020; INTRAE.

CC HSSP: P45697; LSN.

CC IPRC01614; Knot1.

CC InterPro: IPR001219; Neurotoxin.

CC InterPro: IPR02061; Scorpion_toxin_1.

CC PRINS; PR02084; TOXIN.

CC PRODom; PDC00908; Scorpion_toxNL_1.

CC SM005; Knot1.

CC Toxin: Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor.

CC DISULFID 12 65 BY SIMILARITY.

CC DISULFID 16 36 BY SIMILARITY.

CC DISULFID 22 46 BY SIMILARITY.

CC DISULFID 26 48 BY SIMILARITY.

CC SEQUENCE 66 AA; 7453 MN;

CC B5E0DB42237EF2E8 CRC64;

CC Alignment Scores:

CC Pred. No.: 0.0435

CC Score: 76.00

CC Percent Similarity: 56.62%

CC Best Local Similarity: 44.83%

CC Query Match: 26.46%

CC DB: 1

CC US-09-673-274B-2_COPY 1_232 (1-132) x SCXE BUTEY (1-66)

CC Jy 5.2 TCGAACCGTGAGTGCAAGGGGCGGTACAAAGGGTGTCACTGC-----GGTTCC 102

CC Dt 22 CysAspSerGlycLysLysAsr:GlyAlaAspGlySerTyrCysGlnTrpLeuGlyArg 41

CC Qy 10.3 TTGGCTAACGTGAACTGTGGTGTGCGAG 129

CC Db 42 PheGlyAsnAla---CysTrpCysLys 49

CC RESULT 1.5

CC SCL3 LEIQH STANDARD; PRT; 67 AA.

CC AC PSE678;

CC DT 15 JUL 1999 (Rel: 38, Created)

CC DT 15 JUL 1999 (Rel: 38, Last sequence update)

CC DT 15 SEP 2003 (Rel: 42, Last annotation update)

CC LE Alpha-like neurotoxin Lqh III (Lqh3).

CC LEIurus quinquestratus hebraeus (Ye.-cw scorpion).

CC Eukaryota: Metazoa: Arthropoda: Chelicerata: Arachnida: Scorpiones:

CC Order: Butidae; Suborder: Leurota.

CC NCBI TaxID: 6884;

CC RN 11;

CC SEQUENCE, PHARMACOLOGICAL CHARACTERIZATION, AND BIOASSAY.

CC TISSUE:venom;

CC MEDLINE:9833091; PubMed:9917409;

CC Krimm T., Gilles N., Sautiere P., Stankiewicz M., Peihare M.,

CC Gordon D., Lancelin J.-M.;

CC "NMR structures and activity of a novel alpha-like toxin from the

CC scorpion Leurus quinquestratus hebraeus";

CC C. Moi. Bioi. 285(1):1749-1763(1999).

CC 13;

CC STRUCTURE BY NMR.

CC TISSUE:venom;

CC MEDLINE:9911414; PubMed:9917409;

CC Krimm T., Gilles N., Sautiere P., Stankiewicz M., Peihare M.,

CC Gordon D., Lancelin J.-M.;

CC "NMR structures and activity of a novel alpha-like toxin from the

CC scorpion Leurus quinquestratus hebraeus";

CC C. Moi. Bioi. 285(1):1749-1763(1999).

CC 13;

CC STRUCTURE BY NMR.

CC TISSUE:venom;

CC Krimm T., Trivelli X., Lancelin J.-M.;

CC "A Cis trans isomerism of a non-prolyl peptide bond in Lqh III alpha-

CC like scorpion toxin revealed by solution NMR";

RL Submitted (JUL-2003); to the PDB data bank.

CC --!- FUNCTION: Binds to sodium channels and inhibits the inactivation of the activated channels, thereby blocking neuronal transmission.

CC Active on both insects and mammals but competes for alpha-toxins binding only on cockroach sodium channels.

CC --!- SUBUNIT: Monomer.

CC --!- SUBCELLULAR LOCATION: Secreted.

CC --!- TISSUE SPECIFICITY: Expressed by the venom gland.

CC --!- MISCELLANEOUS: LD₅₀: is 50 mg/kg by intracerebroventricular injection into mice.

CC --!- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.

CC ALPHA_TOXIN SUBFAMILY. ALPHA-LIKE TOXIN SUBCLASS.

CC PDB: 1BMR, 16-FEB-99.

CC PDB: 1FH3, 08-NOV-00.

CC DR InterPro: IPR0264; Knot1.

CC DR Pfam: PF00537; toxin_3_1.

CC DR ProDom: PD000908; Scorpion_toxin_1.

CC DR SMART: SM00505; Knot1; l_1_toxin_1.

CC DR Tox3D: Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor; KW Amidation; 3D-structure.

CC DR Amidation: 3D-structure.

CC DR DISULFID 12 65 BY SIMILARITY.

CC DR DISULFID 16 36 BY SIMILARITY.

CC DR DISULFID 22 46 BY SIMILARITY.

CC DR DISULFID 26 48 BY SIMILARITY.

CC DR DISULFID 28 50 BY SIMILARITY.

CC DR DISULFID 30 52 BY SIMILARITY.

CC DR DISULFID 32 54 BY SIMILARITY.

CC DR DISULFID 34 56 BY SIMILARITY.

CC DR DISULFID 36 58 BY SIMILARITY.

CC DR DISULFID 38 60 BY SIMILARITY.

CC DR DISULFID 40 62 BY SIMILARITY.

CC DR DISULFID 42 64 BY SIMILARITY.

CC DR DISULFID 44 66 BY SIMILARITY.

CC DR DISULFID 46 68 BY SIMILARITY.

CC DR DISULFID 48 70 BY SIMILARITY.

CC DR DISULFID 50 72 BY SIMILARITY.

CC DR DISULFID 52 74 BY SIMILARITY.

CC DR DISULFID 54 76 BY SIMILARITY.

CC DR DISULFID 56 78 BY SIMILARITY.

CC DR DISULFID 58 80 BY SIMILARITY.

CC DR DISULFID 60 82 BY SIMILARITY.

CC DR DISULFID 62 84 BY SIMILARITY.

CC DR DISULFID 64 86 BY SIMILARITY.

CC DR DISULFID 66 88 BY SIMILARITY.

CC DR DISULFID 68 90 BY SIMILARITY.

CC DR DISULFID 70 92 BY SIMILARITY.

CC DR DISULFID 72 94 BY SIMILARITY.

CC DR DISULFID 74 96 BY SIMILARITY.

CC DR DISULFID 76 98 BY SIMILARITY.

CC DR DISULFID 78 100 BY SIMILARITY.

CC DR DISULFID 80 102 BY SIMILARITY.

CC DR DISULFID 82 104 BY SIMILARITY.

CC DR DISULFID 84 106 BY SIMILARITY.

CC DR DISULFID 86 108 BY SIMILARITY.

CC DR DISULFID 88 110 BY SIMILARITY.

CC DR DISULFID 90 112 BY SIMILARITY.

CC DR DISULFID 92 114 BY SIMILARITY.

CC DR DISULFID 94 116 BY SIMILARITY.

CC DR DISULFID 96 118 BY SIMILARITY.

CC DR DISULFID 98 120 BY SIMILARITY.

CC DR DISULFID 100 122 BY SIMILARITY.

CC DR DISULFID 102 124 BY SIMILARITY.

CC DR DISULFID 104 126 BY SIMILARITY.

CC DR DISULFID 106 128 BY SIMILARITY.

CC DR DISULFID 108 130 BY SIMILARITY.

CC DR DISULFID 110 132 BY SIMILARITY.

CC DR DISULFID 112 134 BY SIMILARITY.

CC DR DISULFID 114 136 BY SIMILARITY.

CC DR DISULFID 116 138 BY SIMILARITY.

CC DR DISULFID 118 140 BY SIMILARITY.

CC DR DISULFID 120 142 BY SIMILARITY.

CC DR DISULFID 122 144 BY SIMILARITY.

CC DR DISULFID 124 146 BY SIMILARITY.

CC DR DISULFID 126 148 BY SIMILARITY.

CC DR DISULFID 128 150 BY SIMILARITY.

CC DR DISULFID 130 152 BY SIMILARITY.

CC DR DISULFID 132 154 BY SIMILARITY.

CC DR DISULFID 134 156 BY SIMILARITY.

CC DR DISULFID 136 158 BY SIMILARITY.

CC DR DISULFID 138 160 BY SIMILARITY.

CC DR DISULFID 140 162 BY SIMILARITY.

CC DR DISULFID 142 164 BY SIMILARITY.

CC DR DISULFID 144 166 BY SIMILARITY.

CC DR DISULFID 146 168 BY SIMILARITY.

CC DR DISULFID 148 170 BY SIMILARITY.

CC DR DISULFID 150 172 BY SIMILARITY.

CC DR DISULFID 152 174 BY SIMILARITY.

CC DR DISULFID 154 176 BY SIMILARITY.

CC DR DISULFID 156 178 BY SIMILARITY.

CC DR DISULFID 158 180 BY SIMILARITY.

CC DR DISULFID 160 182 BY SIMILARITY.

CC DR DISULFID 162 184 BY SIMILARITY.

CC DR DISULFID 164 186 BY SIMILARITY.

CC DR DISULFID 166 188 BY SIMILARITY.

CC DR DISULFID 168 190 BY SIMILARITY.

CC DR DISULFID 170 192 BY SIMILARITY.

CC DR DISULFID 172 194 BY SIMILARITY.

CC DR DISULFID 174 196 BY SIMILARITY.

CC DR DISULFID 176 198 BY SIMILARITY.

CC DR DISULFID 178 200 BY SIMILARITY.

CC DR DISULFID 180 202 BY SIMILARITY.

CC DR DISULFID 182 204 BY SIMILARITY.

CC DR DISULFID 184 206 BY SIMILARITY.

CC DR DISULFID 186 208 BY SIMILARITY.

CC DR DISULFID 188 210 BY SIMILARITY.

CC DR DISULFID 190 212 BY SIMILARITY.

CC DR DISULFID 192 214 BY SIMILARITY.

CC DR DISULFID 194 216 BY SIMILARITY.

CC DR DISULFID 196 218 BY SIMILARITY.

CC DR DISULFID 198 220 BY SIMILARITY.

CC DR DISULFID 200 222 BY SIMILARITY.

CC DR DISULFID 202 224 BY SIMILARITY.

CC DR DISULFID 204 226 BY SIMILARITY.

CC DR DISULFID 206 228 BY SIMILARITY.

CC DR DISULFID 208 230 BY SIMILARITY.

CC DR DISULFID 210 232 BY SIMILARITY.

CC DR DISULFID 212 234 BY SIMILARITY.

CC DR DISULFID 214 236 BY SIMILARITY.

CC DR DISULFID 216 238 BY SIMILARITY.

CC DR DISULFID 218 240 BY SIMILARITY.

CC DR DISULFID 220 242 BY SIMILARITY.

CC DR DISULFID 222 244 BY SIMILARITY.

CC DR DISULFID 224 246 BY SIMILARITY.

CC DR DISULFID 226 248 BY SIMILARITY.

CC DR DISULFID 228 250 BY SIMILARITY.

CC DR DISULFID 230 252 BY SIMILARITY.

CC DR DISULFID 232 254 BY SIMILARITY.

CC DR DISULFID 234 256 BY SIMILARITY.

CC DR DISULFID 236 258 BY SIMILARITY.

CC DR DISULFID 238 260 BY SIMILARITY.

CC DR DISULFID 240 262 BY SIMILARITY.

CC DR DISULFID 242 264 BY SIMILARITY.

CC DR DISULFID 244 266 BY SIMILARITY.

CC DR DISULFID 246 268 BY SIMILARITY.

CC DR DISULFID 248 270 BY SIMILARITY.

CC DR DISULFID 250 272 BY SIMILARITY.

CC DR DISULFID 252 274 BY SIMILARITY.

CC DR DISULFID 254 276 BY SIMILARITY.

CC DR DISULFID 256 278 BY SIMILARITY.

CC DR DISULFID 258 280 BY SIMILARITY.

CC DR DISULFID 260 282 BY SIMILARITY.

CC DR DISULFID 262 284 BY SIMILARITY.

CC DR DISULFID 264 286 BY SIMILARITY.

CC DR DISULFID 266 288 BY SIMILARITY.

CC DR DISULFID 268 290 BY SIMILARITY.

CC DR DISULFID 270 292 BY SIMILARITY.

CC DR DISULFID 272 294 BY SIMILARITY.

CC DR DISULFID 274 296 BY SIMILARITY.

CC DR DISULFID 276 298 BY SIMILARITY.

CC DR DISULFID 278 300 BY SIMILARITY.

CC DR DISULFID 280 302 BY SIMILARITY.

CC DR DISULFID 282 304 BY SIMILARITY.

CC DR DISULFID 284 306 BY SIMILARITY.

CC DR DISULFID 286 308 BY SIMILARITY.

CC DR DISULFID 288 310 BY SIMILARITY.

CC DR DISULFID 290 312 BY SIMILARITY.

CC DR DISULFID 292 314 BY SIMILARITY.

PN FR2777568 A1.
 XX 22 OCT 1999.
 DC 13 APR 1998; 98FR-004933.
 FF 15 APR 1998; 98FR-004933.
 PR 15 APR 1998; 98FR-004933.
 XX
 PA (RHON) I RHONE-POULENC AGROCHIMIE.
 XX
 DR 2000-108532/10.
 DR N PSDB, AAZ45692.
 XX
 PT New polycysteine peptides, designated heliomycin, with antifungal or
 PP antibacterial activity, useful in medicine or plant protection.
 XX
 Claim 7: Page 31-32; 46pp; French.
 PS
 XX The present sequence represents the heliomycin peptide. Heliomycin is a
 CC polycysteine peptide with antifungal and/or antibacterial activity,
 CC isolated from the lepidopteron Helicites virescens. Heliomycin peptides
 CC contain the sequence given in AAY54378. The heliomycin peptides are
 CC used as pharmaceuticals for treating or preventing fungal infections
 CC in humans and animals. They may also be used as antifungal agents for
 CC plant protection. Nucleic acid encoding the heliomycin peptides is
 CC used to generate transgenic plants that are resistant to some fungi,
 CC Fusarium culmorum, F. oxysporum and Phytophthora cinnamomi, and for
 CC recombinant production of the peptides.
 XX
 SQ Sequence 44 AA;
 Alignment Scores:
 Pred. No.: 4 466e-27 Length: 44
 Score: 267.00 Matches: 44
 Percent Similarity: 100.00% Conservat: 44
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 23 Gaps: C
 US-C9-673-274B-2_COPY_1_132 (1-132) × ABB76860 (1-44)
 QY 1 GATAAGTTATCGGTTCTGCCTGGTGAACCTACACTCCGATTGAAACGGT 60
 DB 1 AspLysLeuIleGlySerCysValTrpGlyAlaAsnTyrrThrSerAspCysAsnGly 20
 YY 6: GAGTCAGAGGAGGGGTATCAAGGGTGGTACTGGGTTGCTAACGTTAACGTGC 120
 DB 21 GluCysLysArgGlyTyrLysGlySerPheAlaAsnValAsnValAsnCys 40
 CY 121 TGATGCGGACT 132
 DB 4: TrpCysGluThr 44
 RESULT 3
 ABB76868
 ID ABB76868 standard; protein: 44 AA.
 XX
 AC ABB76868;
 XX
 DT 03-JUL-2002 (first entry)
 DE Antifungal/antibacterial peptide pEM23.
 XX
 KW Antifungal; antibacterial; fungicide; heliomycin; human medicine;
 KW veterinary medicine; plant protection; bacterial infection;
 KW fungal infection.
 XX
 CS Helicites virescens.
 XX
 PN WO200206324-A2.
 XX
 PD 24-JAN-2002.
 XX
 PF 05-JUL-2001; 2001WO-FR02164.
 XX
 PR 13-JUL-2000; 2000FR-0009248.
 XX
 PD 19-SEP-2000; 2000FR-0011949.
 XX
 PA (ENTO-) ENTOMED SA.
 PA
 P1 Dimarcq J., Legrain M., Menir L;
 P2
 XX
 KPI; 2002-179779/23.
 XX
 PT New peptide derivatives of heliomycin, useful as antibacterial and
 PT antifungal agents in human or veterinary medicine and agriculture -
 XX
 PS Ciaim 15: Page 57; 100pp; French.
 XX
 CC The present invention relates to peptide derivatives of heliomycin with
 CC antifungal and/or antibacterial activity. The present sequence is one
 CC such peptide. The peptides are useful in human and veterinary medicine
 CC and in plant protection, for control of bacterial and fungal infections.
 CC An antifungal and/or antibacterial composition containing at least one
 CC peptide is also claimed.
 XX
 SQ Sequence 44 AA;
 Alignment Scores:
 Pred. No.: 4 466e-27 Length: 44
 Score: 267.00 Matches: 44
 Percent Similarity: 100.00% Conservat: 44
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 23 Gaps: C
 US-C9-673-274B-2_COPY_1_132 (1-132) × ABB76860 (1-44)
 QY 1 GATAAGTTATCGGTTCTGCCTGGTGAACCTACACTCCGATTGAAACGGT 60
 DB 1 AspLysLeuIleGlySerCysValTrpGlyAlaAsnTyrrThrSerAspCysAsnGly 20
 YY 6: GAGTCAGAGGAGGGGTATCAAGGGTGGTACTGGGTTGCTAACGTTAACGTGC 120
 DB 21 GluCysLysArgGlyTyrLysGlySerPheAlaAsnValAsnValAsnCys 40
 CY 121 TGATGCGGACT 132
 DB 4: TrpCysGluThr 44
 RESULT 3
 ABB76868
 ID ABB76868 standard; protein: 44 AA.
 XX
 AC ABB76868;
 XX
 DT 03-JUL-2002 (first entry)
 DE Antifungal/antibacterial peptide pEM23.
 XX
 KW Antifungal; antibacterial; fungicide; heliomycin; human medicine;
 KW veterinary medicine; plant protection; bacterial infection;
 KW fungal infection.
 XX
 CS Helicites virescens.
 XX
 PN WO200206324-A2.
 XX
 PD 24-JAN-2002.
 XX
 PF 05-JUL-2001; 2001WO-FR02164.
 XX
 PR 13-JUL-2000; 2000FR-0009248.
 XX
 PD 19-SEP-2000; 2000FR-0011949.
 XX

| | |
|----------|---|
| PA | (ENTO-) ENTOMED SA. |
| CX | Dimarcq J, Legrain M, Menin L; |
| P1 | |
| P2 | |
| RW | WPI: 2002-179779/23. |
| CX | New peptide derivatives of heliomycin, useful as antibacterial and antifungal agents in human or veterinary medicine and agriculture - |
| PT | Claim 15; Page 57; 100pp; French. |
| CX | The present invention relates to peptide derivatives of heliomycin with antifungal and/or antibacterial activity. The present sequence is one such peptide. The peptides are useful in human and veterinary medicine and in plant protection, for control of bacterial and fungal infections. An antifungal and/or antibacterial composition containing at least one peptide is also claimed. |
| PS | |
| CX | Sequence 44 AA: |
| QQ | Alignment Scores: Aligned. No.: 4.66e-27 Length: 44 Score: 267.00 Matches: 44 Percent Similarity: 100.00% Conservative: 0 Best Local Similarity: 100.00% Mismatches: 0 Query Match: 100.00% Indels: 0 DB: 23 Gaps: 0 |
| DS | JJS-09-673-274B-2_COPY_1_132 (1-132) x ABB76868 (1-44) |
| Dy | 1 GATAAGCTTATCGTTTCGTTGGGTGGGTGACTACACTCCGATTGAAACGGT 60 |
| Db | 1 AspLysLeuIleGlySerCysValTrpGlyAlaValAsnTyrThSerAspCysGly 20 |
| QY | 61 GAGTGCAGAAGGGGGGTACAGGGGGTCACTGGTCACTGGTCTTCGCTAACGTGAATGTC 120 |
| Db | 21 GlucylsSargArgGlytyrLysGlyHisCysGlySerPheAlaAsnValAsnCys 40 |
| Dy | 121 TGGTGGGAGCT 132 |
| Db | 41 TrpCysGluThr 44 |
| RESULT 4 | |
| AA | AY54374 standard; Peptide, 49 AA. |
| XX | AAY54374; |
| DT | 06 APR-2000 (first entry) |
| DD | Amino acid sequence of a fusion peptide of MF-alpha1/heliomycin. |
| DE | Mat alpha1 factor; MF-alpha1; heliomycin; polycysteine peptide; antifungal; antibacterial; fungal infection; plant protection; animal protection; transgenic plant; fungi; bacteria; Cercospora beticola; Cladosporium herbarum; Fusarium culmorum; F. oxysporum; Phytophthora cinnamomi. |
| AC | Chimeric - Saccharomyces cerevisiae. |
| AC | Chimeric - Helicomyces cerevisens. |
| OS | |
| OS | |
| XX | Key Location/Qualifiers |
| FH | Peptide 1..5 |
| FT | /note* "residues derived from the yeast Mat-alpha1 (MF-alpha1) factor" |
| FT | Peptide 6..49 |
| FT | /note= "heliomycin residues" |
| XX | FR2777568-A1. |
| PN | |
| XX | 22-OCT-1999. |
| PD | |
| PF | 98FR-0004933. |

Claim 15; Page 57; 100pp; French

The present invention relates to peptide derivatives of heliomicine with antifungal and/or antibacterial activity. The present sequence is one such peptide. The peptides are useful in human and veterinary medicine and in plant protection, for control of bacterial and fungal infections. An antifungal and/or antibacterial composition containing at least one peptide is also claimed.

Sequence 44 AA;

| Alignment Scores: | Length: | Matches: | Conservative: | Mismatches: | Indels: | Gaps: |
|---|---|-------------------------|---|-------------|---------|-------|
| ed. No.: Score: Percent Similarity: at Local Similarity: Query Match: 23 | 1.11e-26 264 00 100.00% 97.73% 98.88% | 44 43 - 0 0 | Length: 44 Matches: 43 Conservative: - Mismatches: 0 Indels: 0 Gaps: 0 | | | |

-09-673-274B-2_COPY_1_132 (1-132) x ABB76864 (1-44);

```

1 GATAAGCTTATCGGTCCGTGGTGGGGTGACTACACTTCCGATTGCCAACGGT 60
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
1 AspysLleIleGlySerCysValTrpGlyAlaValAsnValTyrThrAspCysAsnIly 20
61 GAGTCCAAGAGGACGGCGTTACAACGGTGTCACTGGGTTCCTTCGCTAACCTGAACTGC 120
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|
21 GlucysLysArgArgGlyTyrLysGlyIyHsCysGlySerPheAlaAsnValAsnCys 40
121 TGGGCCGAGACT 132
|||:|||||:|||||:|
41 TrpCysGluThr 44

```

DULT 8
ABB76872 Standard; Protein: 44 AA.

ABB76872;
03-JUL-2002 (first entry)

Antifungal/antibacterial peptide PEM21.

Antifungal: antibacterial; fungicide; heliomicine; human medicine; veterinary medicine; plant protection; bacterial infection; fungal infection.

Synthetic.

WO200206324-A2.
24-JAN-2002.
05-JUL-2001; 2001WO-FR02164.
13-JUL-2000; 2000FR-0009248.
19-SEP-2000; 2000FR-0011949.
(ENTO-) ENTOMED SA.

Dimarcq J. Legrain M. Menin L;
WPI; 2C02-179779/23.

New peptide derivatives of heliomicine, useful as antibacterial and antifungal agents in human or veterinary medicine and agriculture -

Claim 15; Page 57; 100pp; French.

The present invention relates to peptide derivatives of heliomicine with antifungal and/or antibacterial activity. The present sequence is one such peptide. The peptides are useful in human and veterinary medicine and in plant protection, for control of bacterial and fungal infections. An antifungal and/or antibacterial composition containing at least one peptide is also claimed.

and in plant protection, for control of bacterial and fungal infections. An antifungal and/or antibacterial composition containing at least one peptide is also claimed.

| | | |
|---|--|-----------------|
| X | Sequence | 44 AA; |
| Q | Alignment Scores: | |
| Y | core: 1.17e-26 | Length: 44 |
| Y | core: 264.00 | Matches: 43 |
| C | Percent Similarity: 40.00% | Conservative: 1 |
| C | Best Local Similarity: 97.73% | Mismatches: 0 |
| X | Query Match: 99.88% | Indels: 0 |
| X | B: 23 | Gaps: 0 |
| X | Sequence S-09-673-274B-2_CCPY_1_132 (1-132) x A3B76872 (1-44) | |
| X | BBB76896 standard; Protein: 44 AA. | |
| X | ABB76896; | |
| X | 03-JUL-2002 (first entry) | |
| X | ES60LT ⁹ | |
| X | Antifungal/antibacterial peptide #3. | |
| X | Antifungal; antibacterial; fungicide; helimicine; human medicine; veterinary medicine; plant protection; bacterial infection; fungal infection. | |
| X | Synthetic. | |
| X | WO200206124-A2. | |
| D | 24-JAN-2002. | |
| X | 05-JUL-2001; 2001WO-FR2164. | |
| X | 13-JUL-2000; 2000CFR-3329248. | |
| R | 19-SEP-2000; 2000CFR-3C:1949. | |
| X | (EKTG-) ENTOKED SA. | |
| X | Dimarcq J, Segrain M, Verin L; | |
| I | WPI: 2C02-179779/23. | |
| X | New Peptide derivatives of helimicine, useful as antibacterial and antifungal agents in human or veterinary medicine and agriculture Disclosure; Page 88; 100pp; French. | |
| X | The present invention relates to peptide derivatives of helimicine with antifungal and/or antibacterial activity. The present sequence is one such peptide. The peptides are useful in human and veterinary medicine and in plant protection for control of bacterial and fungal infections. An antifungal and/or antibacterial composition containing at least one peptide is also claimed. | |
| X | Sequence 44 AA; | |

Thu Oct 16 17:43:30 2003

usb-09-673-274b-2_copy_1_132.rag

Page 9

earch completed: October 16, 2003, 17:10:36
ob time : 41.7841 SECs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

M nucleic - protein search, using frame_plus_n2p model

run on: October 16, 2003, 17:06:33 : Search time: 11.2292 Seconds

(without alignments)
1415.504*Million cell updates/sec

title: US-09-673-274B-2

perfect score: 324

sequence: 1 gataaqtatcgatccgtg.....gaacgtgtcgaaaggatccgg 169

scoring table: BL0SOM62

Xgapext 10.0 Xgapext 0.5
Ygapext 10.0 Ygapext 0.5
Fgapext 6.0 Fgapext 7.0
Delet 6.0 Delet 7.0

searched: 127663 seqs, 47026705 residues

total number of hits satisfying chosen parameters: 255726

minimum DB seq length: 0

maximum DB seq length: 2000000000

post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

command line parameters:

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DB=SwissProt_41-QMT=fasian -SUFFIX=1EP -MINMA=FCH=C; -LOOPCL=F -LOOPEXT=0_
UNITS=BITS -PART=1 -END=-1 -MATRIX=blossom62 -TRANS=nroman0.cdi -LSI=45
DOCALIGN=200 -THR SCORE=EDCT -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
OUTPFT=pcl -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
USER=907613624 @CGR 1..36 (run at 16162003 170627_2531 -CPU=6 -ICPU=3
NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELEXT=7
SwissProt_41.*
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database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| result | No. | Score | Query | Match | Length | DB | ID | Description |
|--------|------|-------|-------------------|-------|--------|------------|----|---------------------|
| 1 | 267 | 82.4 | P8154 heliothis v | 44 | 1 | DEFN HBV1 | | P13488 burhus occi |
| 2 | 86 | 26.5 | | 66 | 1 | SCX3_BUTOM | | Q9uac9 mesobuthus |
| 3 | 94.1 | 26.1 | | 85 | 1 | SCN2_MEWSA | | Q9bkj1 mesobuthus |
| 4 | 84 | 25.9 | | 85 | 1 | SCAS_MEWSA | | P09982 burhus occi |
| 5 | 83.5 | 25.8 | | 85 | 1 | SCN3_MEWSA | | P09982 burhus occi |
| 6 | 79.5 | 24.5 | | 66 | 1 | SCXC_CENLL | | Q9bkj0 mesobuthus |
| 7 | 79 | 24.4 | | 85 | 1 | SCXE_BUTOC | | P45657 centruroides |
| 8 | 78.5 | 24.2 | | 65 | 1 | SCX4_BUTOM | | Q17254 burhus occi |
| 9 | 78.5 | 24.2 | | 84 | 1 | SCX3_ANDAU | | P59354 butrus occi |
| 10 | 77.5 | 23.9 | | 64 | 1 | SCU3_LEIQU | | P01480 androctonus |
| 11 | 77.5 | 23.9 | | 65 | 1 | SCX4_LEIQU | | P59356 leurus qui |
| 12 | 77 | 23.8 | | 85 | 1 | SCAT_MEWSA | | P01489 leurus qui |
| 13 | 76.5 | 23.6 | | 61 | 1 | SIX2_MEWSA | | P98555 leurus qui |
| 14 | 76 | 23.5 | | 66 | 1 | SCXE_BUTEU | | P09982 burhus occi |
| 15 | 76 | 23.5 | | 67 | 1 | SCU3_LEIQU | | Q9bkj8 leurus qui |
| 16 | 75.5 | 23.3 | | 84 | 1 | SCXA_MEWSA | | O61705 mesobuthus |
| 17 | 75 | 23.1 | | 84 | 1 | SCX4_ANDAU | | P45658 androctonus |
| 18 | 74.5 | 23.0 | | 70 | 1 | DMYC_DROME | | P4964 drosophila |

ALIGNMENTS

SCX1_CENSC
SCX5_CENSC
P01492 centruroides
P58779 centruroides
P81504 androctonus
P01481 leurus qui
Q9gng8 mesobuthus
Q9gyx2 mesobuthus
P80962 butacus a.
P55903 butus occi
P5594 butus occi
P5664 centruroides
P45697 mesobuthus
P01495 centruroides
Q95wc9 centruroides
Q9nics mesobuthus
P82814 butus simus
P01488 butus occi
P56743 androctonus
P09981 butus europeus
O65740 capsicum annuum
Q9njc4 mesobuthus
P01479 androctonus

SCX1_CENSC
SCX2_CENSC
SCX3_CENSC
SCIO_MEWSA
SC17_MEWSA
SCM2_MEWSA
SC16_MEWSA
SCX6_CERNO
SCX1_MEWSA
SCX2_CENNO
SCX3_CENSC
SCIO_MEWSA
SC14_BUTSI
SCX1_BUTOC
SCX6_ANDAJ
SCX9_BUTEU
SC17_MEWSA
SCX2_ANDAU

SCX1_CENSC
SCX2_CENSC
SCX3_CENSC
SCIO_MEWSA
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SCM2_MEWSA
SC16_MEWSA
SCX6_CERNO
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SCX2_CENNO
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SCX9_BUTEU
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SCX9_BUTEU
SC17_MEWSA
SCX2_ANDAU

SCX1_CENSC
SCX2_CENSC
SCX3_CENSC
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SC17_MEWSA
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SCX1_CENSC
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SCX9_BUTEU
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SCX2_ANDAU

SCX1_CENSC
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SCX2_ANDAU

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SCX2_CENSC
SCX3_CENSC
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SC17_MEWSA
SCM2_MEWSA
SC16_MEWSA
SCX6_CERNO
SCX1_MEWSA
SCX2_CENNO
SCX3_CENSC
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SCX9_BUTEU
SC17_MEWSA
SCX2_ANDAU

SCX1_CENSC
SCX2_CENSC
SCX3_CENSC
SCIO_MEWSA
SC17_MEWSA
SCM2_MEWSA
SC16_MEWSA
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SCX1_MEWSA
SCX2_CENNO
SCX3_CENSC
SCIO_MEWSA
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SCX1_BUTOC
SCX6_ANDAJ
SCX9_BUTEU
SC17_MEWSA
SCX2_ANDAU

SCX1_CENSC
SCX2_CENSC
SCX3_CENSC
SCIO_MEWSA
SC17_MEWSA
SCM2_MEWSA
SC16_MEWSA
SCX6_CERNO
SCX1_MEWSA
SCX2_CENNO
SCX3_CENSC
SCIO_MEWSA
SC14_BUTSI
SCX1_BUTOC
SCX6_ANDAJ
SCX9_BUTEU
SC17_MEWSA
SCX2_ANDAU

SCX1_CENSC
SCX2_CENSC
SCX3_CENSC
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T 28-FEB-2003 (Rel. 41, Last annotation update)

T Neurotoxin AS precursor.

S Mesobuthus martensii (Manchurian scorpion) (Buthus martensii)

C Buthoidea; Arthropoda; Chelicerata; Arachnida; Scorpiones;

C NCBI_TaxID=34649;

X [1]

P P

SEQUENCE FROM N.A.

C TISSUE=Venom gland;

C Lan Z.D., Dai L., Chi C.-W.;

C "The gene cloning and sequencing of AS and AS-1, two novel neurotoxins from the scorpion Buthus martensi Karsch.",

C Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.

C -!- FUNCTION: Ryanodine receptor agonist in skeletal muscle.

C -!- SUBCELLULAR LOCATION: Secreted (By similarity).

C -!- TISSUE SPECIFICITY: Expressed by the venom gland.

C -!- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.

C -!- ALPHA-TOXIN SUBFAMILY.

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C EMBL: AF079060; AAD47374.1; -.

C HSSP: P01492; 1VNB.

C InterPro: IPR003614; Knot1.

C InterPro: IPR002061; Scorpion_toxin1L.

C Pfam: PF00537; toxin_3.

C Prodrom: PD000905; Scorpion_toxin1L; 1.

C SMART: SM00505; Knot1.

C R Toxin; Neurotoxin; Signal.

C T SIGNAL 1 19 POTENTIAL.

C T CHAIN 20 85 NEUROTOXIN AS.

C T DISULFID 31 81 BY SIMILARITY.

C T DISULFID 35 56 BY SIMILARITY.

C T DISULFID 42 63 BY SIMILARITY.

C T DISULFID 46 65 BY SIMILARITY.

C Q SEQUENCE 85 AA; 9759 MW;

C 41286f9DDCD4FE90 CRC64;

C Alignment Scores:

C Pred. No.: 0.0161

C core: 84.00

C Percent Similarity: 55.81%

C Best Local Similarity: 44.19%

C Identity Match: 25.93%

C B: 1

C Gaps: 2

C Length: 85

C Matches: 19

C Conservative: 5

C Mismatches: 17

C Indels: 2

C Pairs: 1

C Potential Scores:

C Pred. No.: 0.3186

C Score: 83.5C

C Percent Similarity: 55.26%

C Best Local Similarity: 42.11%

C Query Match: 25.77%

C DB: 2

C SQ SEQUENCE 85 AA; 9271 MW;

C CID6C93A2F82F8C2 CRC64;

C Alignment Scores:

C Qy 1 GATAAGCTTATCGGTTCCTGGCTGTTGGTGAACACTACACTTCGATTGCCAACGGT 60

C Db 26 AspLysTyrThrGlycylsValTyrPcysValleAsnGluSer--CysSerSer 44

C Qy 61 GAGTGCAAGAGGGGTACAGGGTGTACTGGTTCTTGTCACTGTGACTGC 120

C Db 45 GluCysBystyleArgGlyGlyTyrTyrGlyTyrCys---TyrPheTrpLysLeuAlaCys 63

C Qy 121 TGTGCCAG 129

C Db 64 PheCysGln 66

C AC CN3_MESMA STANDARD; PRT; 85 AA.

C AC Q9BKJ0; Q9GZC4; Created

C DT 28-FEB-2003 (Rel. 41, Last sequence update)

C DT 28-FEB-2003 (Rel. 41, Last annotation update)

C DE peptide).

C OS *Mesobuthus martensi* (Manchurian scorpion) (*Butthus martensi*).

C OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;

C OC Buthoidea; Buthidae; Mesobuthus.

C OX NCBI_TaxID=34649;

C RN [1]

C RP SEQUENCE FROM N.A.

C RC TISSUE=Venom gland;

C RA Zhang J.-H., Hua Z.C., Zhu D.X.;

C RT "Cloning of anti-epilepsy peptide cDNA from scorpion *Butthus martensi*."

C RT Karsch ;

C RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.

C RN [2]

C RP SEQUENCE FROM N.A.

C RC TISSUE=Venom gland,

C RA Zhang J.-H., Hua Z.C., Zhu D.X.;

C RT "Cloning of anti-neuroexcitation peptide III (ANEPI) cDNA from scorpion *Butthus martensi* Karisch."

C RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

C CC -!- FUNCTION: Binds to sodium channels and inhibits them.

C CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).

C CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.

C CC -!- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.

C CC -!- ALPHA-TOXIN SUBFAMILY.

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C CC EMBL: AF22003; AAC01571.1; -.

C DR EMBL: AF224273; AAC28342.1; -.

C DR HSSP: PG1494; 2SN3

C DR InterPro: IPR003614; Knot1.

C DR Pfam: PF00537; toxin_3.

C DR ProDom: P00C30B; Scorpion_toxin1L.

C DR SMART: SM00505; Knot1.

C DR Toxin; Neurotoxin; Signal.

C FT SIGNAL 1 21 POTENTIAL.

C FT CHAIN 22 85 ANTI-NEUROEXCITATION PEPTIDE III.

C FT DISULFID 31 81 BY SIMILARITY.

C FT DISULFID 35 56 BY SIMILARITY.

C FT DISULFID 42 63 BY SIMILARITY.

C FT DISULFID 46 65 BY SIMILARITY.

C FT CONFLICT 47 K->I (IN REF. 2)

C SQ SEQUENCE 85 AA; 9271 MW;

C CID6C93A2F82F8C2 CRC64;

C Alignment Scores:

C Pred. No.: 0.3186

C Score: 83.5C

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C Alignment Scores:

C Pred. No.: 0.3186

C Score: 83.5C

C Percent Similarity: 55.26%

C Best Local Similarity: 42.11%

C Query Match: 25.77%

C DB: 2

AC P45667; MEDLINE=96300228; PubMed=8706664;
 ET 01-NOV-1995 (Rel. 32, Created)
 ET 01-NOV-1995 (Rel. 32, Last sequence update)
 ET 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Crustacean-specific toxin 1.
 CS Centruroides limpidus (Mexican scorpion).
 OC Eukaryota; Metazoa; Arthropoda; Chelicera; Arachnida; Scorpiones;
 OC Buthoidea; Butidae; Centruroides.
 CX NCBI_TaxID=29941;
 RN [1];
 RP SEQUENCE, DISULFIDE BONDS, AND STRUCTURE BY NMR.
 RC TISSUE=venom;
 RX MEDLINE=9524424; PubMed=7727365;
 RA Lebreton F., Deleperre M., Ramirez A.N., Balderas C., Possani L.D.;
 RT "Primary and NMR three-dimensional structure determination of a novel
 crustacean toxin from the venom of the scorpion Centruroides limpidus
 limpidus Karsh.";
 RL Biochemistry 33:11135-11149(1994).
 CC !- FUNCTION: Binds to sodium channels and inhibits the inactivation
 CC of the activated channels, thereby blocking neuronal transmission.
 CC !- SUBCELLULAR LOCATION: Secreted.
 CC !- TISSUE SPECIFICITY: Expressed by the venom gland.
 CC !- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.
 CC PIR: A55869; A55899.
 DR HSSP; P01492; JVB; Knoti.
 DR InterPro: IPR003614; Knoti.
 DR InterPro: IPR001219; Neurotoxin.
 DR InterPro: IPR002361; Scorpion_toxinL.
 PTx; PROJ537; toxin 3; i.
 PRNTS; PROC284; TOXIN
 PRODOM; P000928; Scorpion_toxinL; 1.
 DR SMART; SMC0505; Knoti; 1.
 KW Toxin; Neurtoxin; Ionic channel inhibitor; Sodium channel inhibitor;
 KW Signal.
 FT DISULFID 12 65 Length: 66
 FT DISULFID 16 41 Matches: 17
 FT DISULFID 25 46 Conservative: 4
 FT DISULFID 29 48 Mismatches: 1
 SQ SEQUENCE 66 AA: A478E63796F54DAA CRC64;
 US 09 673 274B-2 (1-169) × SCXE_CENLL (1-66);
 Alignment Scores:
 Pred. No.: 0.0571; Length: 66
 Score: 79.50; Matches: 17
 Percent sim.: 85%; Conservative: 4
 Best Local Similarity: 43.59%; Mismatches: 1
 Query Match: 24.54%; Index: 7
 DB: 1 Gaps: 3
 US 09 673 274B-2 (1-169) × SCXE_BUTOC (1-86);
 Qy 19 TGGCTGGGGTGTGAACTACACTCCGATGCAACGGTAGTGAGTCAGGGGGT 78
 Db 16 CysPheTripleGlyLysAsn-----GluAsnCysAspLysAlaLysAsn 33
 Qy 79 TACAGGT-----GGTACTGCCTGCTCTGCTAACGTGAACTGTGTCGAG 129
 Db 34 GluGlyGlySerTyroCystySerPheAla-----CystPcysGlu 49
 RESULT 7
 SCXE_BUTOC STANDARD; PRT; 85 AA.
 AC Q17254; ID SCX4_BUTOC STANDARD; PRT; 65 AA.
 DT 15-DEC-1998 (Rel. 37, Created); AC P59355;
 DT 15-DEC-1998 (Rel. 37, Last sequence update); DT 28-FEB-2003 (Rel. 41, Created);
 DT 28-FEB-2003 (Rel. 41, Last annotation update); DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Neurotoxin XIV precursor (Bor14).
 CS Buthoidea; Centruroides tunecanus (Common European scorpion).
 OC Eukaryota; Metazoa; Arthropoda; Chelicera; Arachnida; Scorpiones;
 OC Buthoidea; Butidae; Buthus.
 NCBI_TaxID=6871;
 RN [1];
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom;

SC-26 LEICH: STANDARD; PRT; 64 AA.
 AC 259 Feb 2003 (Rel. 4); Created;
 DT 25-FEB-2003 (Rel. 4); Last sequence update;
 DT 25-FEB-2003 (Rel. 4); Last annotation update;
 DE Alpha-like neurotoxin (Lqg VI (Lqg6)).
 OS *Leurus quinquestriatus hebraeus* (Yellow scorpion).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Buthidae; Leiurus;
 OX NBI_TaxID=6884;
 RN 11
 RP SEQUENCE: PHARMACOLOGICAL CHARACTERIZATION, AND BIASSAY.
 KC TISSUE: Venom;
 XC MEDLINE:216983; PubMed=121896;
 RX Hatch A., Gilles N., Sautiere P., Martineau A., Kopeyan C., Udens C.,
 RA "Yugat J.", Lance, in J.-M., Gordon D.;
 RA "Characterization of scorpion alpha-like toxin group using two new
 toxins from the scorpion *Leurus quinquestriatus hebraeus*.";
 RT Eti. J. Biochem. 269:3920-3933(2002)
 RL LD₅₀: 34.3 nmol/kg to cockroaches (Bacitella
 CC :); FUNCTION: Binds to sodium channels and inhibits the inactivation
 of the activated channels, thereby blocking neuronal transmission.
 CC This toxin is highly toxic to insects and mice and inhibits the
 binding of alpha-toxin to cockroach neuronal membranes.
 CC SUBCELLULAR LOCATION: Secreted.
 CC TISSUE SPECIFICITY: Expressed by the venom gland.
 CC :); MISCELLANEOUS: LD₅₀: 34.3 nmol/kg to cockroaches (Bacitella
 KW :); SEMANTICAL:
 CC :); SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.
 CC :); ALPHATOXIN SUBFAMILY: ALPHA-LIKE TOXIN SUBCLASS.
 DR plant; UP3C537; toxin3; 1.
 DR PRODOM: PC000908; Scorpion_toxin; 1.
 DR SMART: SM00505; Knot1; 1.
 DR Toxin; Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor;
 KW Amidation.
 PT DISULFID 12 BY SIMILARITY.
 PT DISULFID 16 BY SIMILARITY.
 PT DISULFID 20 BY SIMILARITY.
 PT DISULFID 24 BY SIMILARITY.
 PT MOD RES 64 BY AMIDATION.
 SQ SEQUENCE: 64 AA; 6803 MW; 49A54B03C75392E CRC64;
 Alignment Scores:
 Pred. No.: 0.101 Length: 64
 Score: 77.50 Matches: 15
 Percent Similarity: 51.84 Conservative: 5
 Best Local Similarity: 38.46% Mismatches: 14
 Query Match: 23.92% Indels: 5
 DB: 1 Gaps: 2
 US-09-673-274B-2 (1-169) × SCX4 LEIQU (1-64)
 PT 16 TCCTGGTGTGCG-----GGTGCTGTGAACCTACACTTCGATTGAGTGCAGTCAG 69
 PT 12 AsnCysValTyrThrCysGlySerAsnSerTy-----CysAsnThrGluCysThr 28
 DB 12 AsnCysValTyrThrCysGlySerAsnSerTy-----CysAsnThrGluCysThr 28
 OY 70 AGGAGGGTTACAAGGTGTYCAGTCG-----GTTCTCTTCGTAACGTCG 120
 DB 29 LysAsnGlyAlaGluSerGlyTyrCysGlnTripleGlyLysTrpGlyAsnAla---Cys 47
 DB: 121 TGGTGC 126
 OY 121 TGGTGC 126
 DB 48 TrpCys 49
 RESULT 12
 SCAT_MESMA STANDARD; PRT; 85 AA.
 ID SCAT_MESMA STANDARD;
 AC Q9UAC8;
 DT 28-FEB-2003 (Rel. 4); Created;
 DT 28-FEB-2003 (Rel. 4); Last sequence update;
 DT 28-FEB-2003 (Rel. 4); Last annotation update;
 DE Neurotoxin AS-1 precursor.
 OS Mesobuthus martensii (Manchurian scorpion) (*Buthus martensii*).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Buthidae; Mesobuthus.
 OX NCBI_TaxID=34649;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE:Venom Gland;
 RA Lan Z.-D., Dai L., Chi C.-W.;
 RT "The gene cloning and sequencing of AS and AS-1, two novel neurotoxins
 from the scorpion *Buthus martensii* Karsch.";
 RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
 CC :); FUNCTION: Rydine receptor agonist in skeletal muscle.
 CC :); SUBCELLULAR LOCATION: Secreted (By similarity).
 CC :); TISSUE SPECIFICITY: Expressed by the venom gland.
 CC :); SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.
 RN 11
 SCX4 LEIQU STANDARD; PRT; 65 AA.
 AC P01485;
 DT 21-JUL-1986 (Rel. 0); Created;
 DT 21-JUL-1986 (Rel. 0); Last sequence update;
 DT 26-FEB-2003 (Rel. 4); Last annotation update;
 DE Leurus quinquestriatus hebraeus (Egyptian scorpion).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Buthidae; Leiurus;
 OX NCBI_TaxID=6885;
 RN 11
 SEQUENCE:

| | | |
|----|---|--|
| IC | ALPHA-TOXIN SUBFAMILY. | |
| IC | This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). | Chemistry, action, and gene cloning"; ". |
| IC | EMBL: AF079061; AAD41375.1; -; | RN [3]. |
| OR | HSSP; P01492; 1YNB. | RL Arch. Insect Biochem. Physiol. 22:55-73(1993). |
| OR | InterPro: IPR03614; Knot1. | RN [3]. |
| OR | Pfam: PF00357; toxin_1; 1. | RP ACTION. |
| OR | ProdDom; PDD002061; Scorpion_toxinL; 1. | RA Zlotkin E., Fowler E., Etian M., Moyer M., Adams M.E.; |
| OR | SMART: SM00505; Knot1; 1. | RA "On the chemistry and action of the depressant insect toxin"; |
| OR | TOXIN; Neurotoxin; Signal. | RT Toxicon 28:170-170(1993). |
| IC | SEQUENCE: 1 19 POTENTIAL. NEUROTOXIN AS-1. | CC -!- FUNCTION: Binds to sodium channels and inhibits the inactivation of the activated channels, thereby blocking neuronal transmission. |
| IC | T CHAIN 20 85 NEUROTOXIN AS-1. | CC This toxin induces a slow, depressant, flaccid paralysis on fly larvae. It is active only on insects. |
| IC | T DISULFID 31 81 BY SIMILARITY. | CC -!- SUBCELLULAR LOCATION: Secreted. |
| IC | T DISULFID 35 56 BY SIMILARITY. | CC -!- TISSUE SPECIFICITY: Belongs to THE ALPHA/BETA-SCORPION TOXIN FAMILY. |
| IC | T DISULFID 42 63 BY SIMILARITY. | CC -!- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN. |
| IC | T DISULFID 46 65 BY SIMILARITY. | CC -!- TISSUE SPECIFICITY: Expressed by the venom gland. |
| IC | Q SEQUENCE 85 AA: E2274838439E2B95 CRC64; | CC -!- ALPHA-TOXIN SUBFAMILY. |
| IC | Alignment Scores: | |
| IC | red. No.: core: 0.119 Length: 85 | CC HSSP: PC1494; 2SN3. |
| IC | percent Similarity: 77.00 Matches: 17 | DR InterPro: IPR0C3614; Knot1. |
| IC | est Local Similarity: 53.49% Conservative: 6 | DR Pfam: PF00537; toxin_1; 1. |
| IC | very Match: 23.77% Mismatches: 18 | DR ProdDom: PDD00505; Knot1; 1. |
| IC | B: 1 Gaps: 2 | DR SMART: SM00505; Knot1; 1. |
| IC | Y S-09-673-274B-2 (1-169) x SCAT_MESNA (1-85) | KW Toxin: Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor. |
| IC | b 1 GATAAGTTATCGGTTCTCGGTGGGGTGTGAACATTCGGATTGCCAACGGT 60 | FT DISULFID 16 60 BY SIMILARITY. |
| IC | b 26 AsnLysTyrThrGlyCysLysIleTerpcysValLeasnGluSer--CysSerSer 44 | FT DISULFID 14 35 BY SIMILARITY. |
| IC | b 61 GACTGCAGAGGGGGTACAAGGGGGTCACTGGGTCTCTTCTAACTGTGAACTGC 120 | FT DISULFID 21 42 BY SIMILARITY. |
| IC | b 45 G..ucysysLeuarginGlyAsnTyGlyIyrcs--TyrPheTerplysLeuAlaCys 63 | SC SEQUENCE 61 AA: E8C01771C7DCFAF6 CRC64; |
| IC | Y 121 TGCTGCAG 129 | US-09-673-274B-2 (1-169) x SIX2_LEIQU (1-61) |
| IC | b 64 TyrCysGlu 66 | Alignment Scores: |
| IC | Alignment Scores: | Pred. No.: 0.114 |
| IC | core: 77.00 Length: 61 | Score: 76.50 |
| IC | percent Similarity: 53.49% Matches: 15 | Percent Similarity: 55.26% |
| IC | est Local Similarity: 23.77% Conservative: 6 | Best Local Similarity: 39.47% |
| IC | very Match: 23.77% Mismatches: 12 | Query Match: 23.61% |
| IC | B: 1 Gaps: 2 | DB: 1 |
| IC | Y RESULT 14 | DB: 2 |
| IC | SEQUENCE: SCXE_BUTEU STANDARD; PRT: 66 AA. | SCXE_BUTEU STANDARD; |
| IC | D SIX2 LEIQU | PRT: 66 AA. |
| IC | C P09982; ID SCXE_BUTEU | AC P09982; |
| IC | C 01-MAR-1989 (Rel. 10, Created) | CC MEDLINE=0504632; PubMed=6697916; |
| IC | C 01-FEB-1991 (Rel. 17, Last sequence update) | RA Volkova T.M., Garsia A.P., Telezhinskaya I.N., Pottopenko N.A., |
| IC | T 01-FEB-1991 (Rel. 17, Last sequence update) | RA Grishin E.V.; |
| IC | T 28-FEB-2003 (Rel. 41, Last annotation update) | DE Neurotoxin M.A.; |
| IC | E Insect toxin 2 (Insect toxin LqQT2). | OS Butihus eupeus (Lesser Asian scorpion) (Mesobuthus eupeus). |
| IC | S Leirus quinquestriatus quinquestriatus (Egyptian scorpion). | OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones; |
| IC | S Euscorpiida; Butihidae; Butihus. | OC Butihidae; Butihidae; Mesobuthus. |
| IC | C NCBI_TaxID=6885; [1] | OX NCBI_TaxID=34648; |
| IC | N RN [1] | RN [1] |
| IC | P RP SEQUENCE:Venom; | RC TISSUE:Venom; |
| IC | P RC TISSUE:Venom; | RX MEDLINE=0504632; PubMed=6697916; |
| IC | P RA Volkova T.M., Garsia A.P., Telezhinskaya I.N., Pottopenko N.A., | RA |
| IC | P RA Grishin E.V.; | RA |
| IC | P RT "Amiro acid sequence of 2 neurotoxins from the scorpion Butihus eupeus." | RT |
| IC | P RL Bioorg. Khim. 10:979-982(1984); | RT |
| IC | P CC -!- FUNCTION: Binds to sodium channels and inhibits the inactivation of the activated channels, thereby blocking neuronal transmission. | CC |
| IC | P CC This paralytic activity in mice. | CC |
| IC | P CC -!- SUBCELLULAR LOCATION: Secreted. | CC |
| IC | P CC -!- TISSUE SPECIFICITY: Expressed by the venom gland. | CC |
| IC | X X MEDLINE=90184494; PubMed=2211768; | |
| IC | X A Kopeyan C., Mansuelle P., Sampieri F., Brando T., Bahraoui E.M., Rochat H., Granier C.; "Primary structure of scorpion anti-insect toxins isolated from the venom of Leirus quinquestriatus quinquestriatus." FEBS Lett. 261:423-426(1990). | |
| IC | X X MEDLINE=93160530; PubMed=B431601; P SEQUENCE. | |
| IC | X A Zlotkin E., Gurevitz M., Fowler E., Adams M.E.; "Depressant insect selective neurotoxins from scorpion venom." | |

CC :! SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.

CC PIR: CTC220; NTS4E.

DR HSSP: P45697; ISN1.

DR InterPro: IPR0364; Knot1.

DR InterPro: IPR001219; Neurotoxin.

DR InterPro: IPR02061; Scorpion_toxinL.

DR PRODom: PRO0584; TOXIN_1.

DR SMART: SM00508; Scorpion_toxinL_1.

DR Toxin; Neurtoxin; Knot1; Ionic channel inhibitor; Sodium channel inhibitor.

DR DISULFID 12; 65 BY SIMILARITY.

FT DISULFID 16; 36 BY SIMILARITY.

FT DISULFID 22; 46 BY SIMILARITY.

FT DISULFID 26; 48 BY SIMILARITY.

SO SEQUENCE: 66 AA; 7453 MW;

35E0CB42237E:2E8 CRC64;

Alignment Scores:

Pred. No.: 0.155 Length: 66
Score: 76.00 Matches: 13

Percent Similarity: 58.62% Conservative: 4
Best Local Similarity: 44.83% Mismatches: 8

Query Match: 23.46% Inlays: 4
LB: Gaps: 2

US-09-673-274B-2 (1-169); x SCXE_BTUE (1-66)

JY 52 TGCACCGTGAGTGCAGAGGGGTACAAAGGGTGGTCACTGC-----GGTCC 102

LE 22 CysaspSerCysLysLysAspG...yAlaAspISe-TyrCysGinTripleG...Arg 41

JY 103 TTGCTTAAGCTGAAGTCTGCTGGCGAG 129

1st 42 theGlyAspAla...Cys-Cys...Cys 49

RESULT 15

SC3 LEIGH STANDARD; PRT; 67 AA.

AC P56618; 15 JUL 1999 (Rel. 38, Created)

DR 15-JUL-1999 (Rel. 38. Last sequence update)

DR 15-SEP-2003 (Rel. 42. Last annotation update)

DE Alpha-1-like neurotoxin Lqh II; (Lqh3).

OS Leirus quinquestratus hebraeus (Yellow scorpion).

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;

CC Burmese; Burmese; Leirus.

NCBI TaxID: 63684;

CX Sauriere P., Cestele S., Kopyyan C., Martineage A., Drobecq H.,

DA Dolinsky Y., Gordon D.;

"New toxins acting on sodium channels from the scorpion Leirus

quinquestratus hebraeus suggest a clue to mammalian vs insect

selectivity".

JMOL. BIOL. 285:1749-1763(1999).

RN STRUCTURE BY NMR.

RP STRUCTURE BY NMR.

RC TISSUE:Venom;

RX MEDLINE=991414; PubMed=9917409;

RA Krimm I., Gilles N., Sauriere P., Starkeiewicz M., Peihate M.,

RA Gordon D., Lancelin J.-M.,

RA "NMR structures and activity of a novel alpha-like toxin from the

scorpion Leirus quinquestratus hebraeus.",

J. Mol. Biol. 285:1749-1763(1999).

RN STRUCTURE BY NMR.

RC TISSUE:Venom;

RA Krimm I., Trivelli X., Lancein J.-M.;

RA "A cis-trans isomerism of a non-prolyl peptide bond in Lqh II: alpha-

RT like scorpion toxin revealed by solution NMR.";

RL Submitted (JUL-2000) to the PDB data bank.

CC -!- FUNCTION: Binds to sodium channels and inhibits the inactivation of the activated channels, thereby blocking neuronal transmission.

CC Active on both insects and mammals but competes for alpha-toxins.

CC binding only on cockroach sodium channels.

CC -!- SUBUNIT: Monomer.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.

CC -!- MISCELLANEOUS: LD₅₀ is 50 mg/kg by intraabdominal injection into mice.

CC -!- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.

CC ALPHA-TOXIN SUBFAMILY.

CC ALPHA-TOXIN SUBFAMILY.

CC ALPHA-LIKE TOXIN SUBCLASS.

CC PDB: 1BMR; 16-FEB-99.

DR PDB: 1FH3; 08-NOV-00.

DR InterPro: IPR03364; Knot1.

DR Pfam: PF00537; toxin_3; 1.

DR ProDom: PDC009CA; Scorpion_toxin1; 1.

DR SMART: SM0C505; Knot1; 1.

DR Toxin; Neurtoxin; Ionic channel inhibitor; Sodium channel inhibitor.

DR Amidation; 3D-structure.

DR Disulfide; 12; 65

FT Disulfide 16; 37

FT Disulfide 23; 47

FT Disulfide 27; 49

FT MOD_RES 67; 67

FT STRAND 2; 6

FT TURN 9; 11

FT HELIX 21; 3C

FT TURN 31; 31

FT STRAND 34; 43

FT TURN 41; 43

FT STRAND 44; 52

FT TURN 54; 55

FT STRAND 67 AA; 7057 MW; 19FB8EF96154328F CRC64;

Alignment Scores:

Aligned. No.: 0.155

Length: 67

Matches: 14

Score: 76.00

Percent Similarity: 51.28%

Best Local Similarity: 35.90%

Query Match: 23.46%

DB: 1

Mismatches: 5

Indels: 1

Gaps: 1

US-C9-673-274B-2 (1-169); x SC3_LEIQH (1-67)

OY 16 TCTCTGCTGGGGTGTGGTGTGACTACACTCCGATGTTGACAGGGAGGAGGAGG 75

DB 11 AsnCysvalaTyrHisCysPheProGlySerSerGlyCysLysGluLys 30

OY 76 GTTACAGGSGGTGCTACTGGGGTCTTCGCT----AACGTCGAACGCTGTGTC 126

DB 31 GlyGlyThrSerGlyHisCysGlyPhylsValGlyLeuAlaCysTrpCys 49

Search completed: October 16, 2003, 17:07:23

Job time : 12:2292 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2003 Compugen Ltd.

MM nucleic - protein search, using frame_plus_n2p model
 run on: October 16, 2003, 17:06:37 ; Search time 49.9701 Seconds
 (without alignments)
 title: US-09-673-274B-2
 refect score: 34
 sequence: 1 gataaqtatcggttctg,.....,gaaacgtgtcgacggatccgg 169

coring table: BloSUM62
 Xgapext 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delopt 6.0 , Delext 7.0
 searched: 830325 seqs, 25805264 residues
 total number of hits satisfying chosen parameters: 1661050

minimum DB seq length: 0
 maximum DB seq length: 2000000000

post-processing: Minimum Match 0%,
 Maximum Match 100%
 Listing first 45 summaries

command line parameters:
 MODEL=frame_n2p.model DEV=xlp
 Q=cgn2_1/USPTO_spoof/US9673274/runat_16102003_170627_2545/app query.fasta_1.654

DB=SPTREMBL_23 -QFMT=FASTA -SUFFIX=rspt -MINMAX=rpt -LOOPCJ=0 -LOOPEXT=0
 UNITS=blocks -START=1 -END=1
 -MATRIX=Diamond0.cdi -LIST=45
 DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGNN15 -MODEL=LOCAL
 OUTPFT=pfo -NORM=EXT
 NO MMAP -LARGEOUT -NEG SCORE=0 -WAIT -DSBLOCK=100 -LONGLOG
 DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREEDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
 PGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOPT=6 -DELEXT=7

atabase : SPTREMBL_23,*

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rplant:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match Length | DB ID | Description |
|------------|-------|--------------|-------|-------------------|
| 1 | 84.5 | 26.1 | 65 5 | Q17231 mesobuthus |

Q17230 mesobuthus
 0810k7 mesobuthus
 Q9Wx6 mesobuthus
 Q9Y87 mesobuthus
 Q833C mesobuthus
 P82761 arabidopsis
 Q9zq5 drosophila
 Q8mv7 leiusus cui
 Q9ju3 mesobuthus
 Q9i670 leishmania
 Q9vr2 drosophila
 Q8ry4 centruroides
 Q9gu7 mesobuthus
 Q9vz3 drosophila
 Q95p69 mesobuthus
 Q9tpg1 phascolus a
 Q9u60 mytilus gal
 Q9v650 leiusus cui
 Q8mv6 leiusus cui
 Q8mvs8 leiusus cui
 Q9y0a9 mytilus gal
 Q8t3a6 caenorhabditis
 Q8c3a7 caenorhabditis
 Q9xw6 drosophila
 Q8ird6 drosophila
 Q9rzq4 drosophila
 Q9v0b8 mesobuthus
 Q39403 brassica oleracea
 Q9u1k6 drosophila
 Q9w526 drosophila
 Q9rx36 deinococcus
 Q9aq36 homo sapiens
 Q9vh52 mus musculus
 C15038 homo sapiens
 Q6c382 homo sapiens
 Q9uh8 homo sapiens
 Q9uq35 homo sapiens
 Q9ew11 centruroides
 P91904 caenorhabditis
 076963 orthochirids
 Q99h52 nectria rac
 Q9blm4 androctonus
 Q9whf2 agricris seg
 Q9rsb3 drosophila
 Q26292 leiusus cui

ALIGNMENTS

RESULT 1
 Q17231 PRELIMINARY; PRT: 65 AA.
 ID C17231
 AC Q17231;
 DT 01-NOV-1996 (TREMBL); 0; Created
 DT 01-MAR-2003 (TREMBL); 0; Last sequence update
 DT 01-MAR-2003 (TREMBL); 23; Last annotation update
 DE Insect toxin; 2.
 GN IT2
 OS Mesobuthus martensii ('Manchurian scorpion') (Ruthus martensii).
 OC Eukaryota; Metazoa; Anthropoda; Cheliceraata; Arachnida; Scorpiones;
 OC Buthoidea; Butidae; Mesobuthus.
 OX NCBI_TaxID=34649;
 RN [1];
 RP SEQUENCE FROM N.A.
 RC TISSUE="elson;
 RA Zhu X., Zhang T., Zhu Y.;
 RT "Cloning and sequencing of two depressant insect selective neurotoxin cDNAs from *Buthus martensii Karsch*."
 RL Kexue Tongbao 41:1387-1391(1996).
 CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY)
 CC -!- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.
 CC EMBL_X22077; CAA2059_1; -.
 DR HSSP_P01494; 2SN3;
 DR InterPro; IPR003614; Knotl.

| | |
|---|--|
| Qy | 76 CGGTACAGGTGGTCACTGGGTTCTGGTAACGTTAACGTAAGCTGTCGCGAG 129 |
| Db | 30 GlyAlaTyryTyrcysTrpTrpTrp--GlyLeuAlaCysTrpTrpGlu 46 |
| RESULT 3 | |
| Q81OK7 | PRELIMINARY; PRT; 85 AA. |
| AC Q81OK7; | |
| DT 01-MAR-2003 (TREMBLref); 23. Created | |
| DT 01-MAR-2003 (TREMBLref); 23. Last sequence update | |
| DT 01-MAR-2003 (TREMBLref); 23. Last annotation update | |
| DE Depressant scorpion toxin KIM2 precursor. | |
| GN KIM2. | |
| OS Mesobuthus marteissii (Manchurian scorpion) (Butthus martensisii). | |
| OC Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones; Buthoidea; Buthiidae; Mesobuthus. | |
| OC NCBI_TaxID=34649; | |
| OX [1] | |
| RN RP SEQUENCE FROM N.A. | |
| RA MEDLINE=2217688; PubMed=12230558; | |
| RA Peng F., Zeng X.C., He X.H., Pu J., Li W.X., Zhu Z.H., Liu H.; | |
| RT "Molecular cloning and functional expression of a gene encoding an antiarrhythmic peptide derived from the scorpion toxin."; | |
| RU Eur. J. Biochem. 269:4468-4475 (2002). | |
| DR EMBL; AF459791; AAN59782; -. | |
| DR EMBL; AF459792; AAN59783; -. | |
| SO SEQUENCE 85 AA; 9425 MW; 507603B9966AA6F CRC64; | |
| Alignment Scores: | |
| Pred. No.: C_0.043 | length: 85 |
| Score: 81.50 | Matches: 16 |
| Percent Similarity: 55.26% | Conservative: 5 |
| Best Local Similarity: 42.11% | Mismatches: 12 |
| Query Match: 25.77% | Indels: 5 |
| DB: 5 | Gaps: 2 |
| US-09-673-274B-2 (1-169) x Q81OK7 (1-85) | |
| Qy 16 TCCGTGCGGTGGGGTGTGAACTACACTCCGATTGCCAACGGTGAGTCGAAGAGGA | |
| Db 34 SercysLeuTrpTrp-----AsnGluGlyCysAsnLyscIucySlysGlyTrp | |
| Qy 76 GGTTACAGGTGGTCACTGGGTTCTCGCTAACGTAAGCTGTCGCGAG 129 | |
| Db 50 GlyAlaTyryTyrcysTrpTrpTrpTrp--GlyLeuAlaCysTrpTrpGlu 66 | |
| RESULT 4 | |
| Q95WGX6 | PRELIMINARY; PRT; 85 AA. |
| AC Q95WGX6; | |
| DT 01-DEC-2001 (TREMBLref); 19. Created | |
| DT 01-DEC-2001 (TREMBLref); 19. Last sequence update | |
| DT 01-MAR-2003 (TREMBLref); 23. Last annotation update | |
| DE Depressant insect neurotoxin BmK ITB precursor. | |
| OS Mesobuthus marteissii (Manchurian scorpion) (Butthus martensisii). | |
| OC Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones; Buthoidea; Buthiidae; Mesobuthus. | |
| OC NCBI_TaxID=34649; | |
| OX [1] | |
| RN RP SEQUENCE FROM N.A. | |
| RA Wang C., Ling M., Wang D., Chi C.; | |
| RT "The gene for depressant insect toxin BmK ITB from Chinese scorpion Butthus marteissii Karsch." | |
| RU Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases. | |
| CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY). | |
| CC -!- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. | |
| DR EMBL; AF272777; AAF77063; 2; | |
| DR InterPro; IPR003614; Knot1. | |
| DR EMBL; IPR002061; Scorpion_toxinL. | |
| PFAM; PF00537; toxinL; 1. | |
| PRODOM; PD00908; Scorpion_toxinL; 1. | |
| SMART; SM00505; Knot1. | |
| Neurotoxin; Signal1. | |

| | | | | | | | | |
|--|---|----------|------------------------|---------------------------------------|------|--------|--|--|
| TT | SIGNAL | 1 | 21 | POTENTIAL. | | | | |
| CHAIN | 22 | 82 | | DEPRESSANT INSECT NEUROTOXIN BMK IBS. | | | | |
| 3Q SEQUENCE | 85 AA: | 9330 MW: | | 80CD314956DE8C CRC64; | | | | |
| Alignment Scores: | | | | | | | | |
| Refined No.: | 0.0783 | | Length: | 85 | | | | |
| Score: | 81.50 | | Matches: | 15 | | | | |
| Percent Similarity: | 55.26% | | Conservative: | 6 | | | | |
| Best Local Similarity: | 39.47% | | Mismatches: | 12 | | | | |
| Query Match: | 25.15% | | Indels: | 5 | | | | |
| DB: | 5 | | Gaps: | 2. | | | | |
| JS-09-673-274B-2 (1-169) × Q95WX6 (1-85) | | | | | | | | |
| D | Q9XY87 | | PRELIMINARY; | | PRT; | 85 AA. | | |
| AC | Q9XY87; | | | | | | | |
| DT | 01-NOV-1999 (TREMBLre). | 12. | Created | | | | | |
| DT | 01-NOV-1999 (TREMBLre). | 12. | Last sequence update | | | | | |
| DT | 01-MAR-2003 (TREMBLre). | 23. | Last annotation update | | | | | |
| DE | Neurotoxin | | | | | | | |
| DE | Scorpion | | | | | | | |
| DS | Mesobuthus martensii (Manchurian scorpion) | | | | | | | |
| DC | Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones; | | | | | | | |
| DC | Buthidae; Mesobuthus. | | | | | | | |
| NCBI_TaxID=14649; | | | | | | | | |
| DN | SEQUENCE FROM N.A. | | | | | | | |
| DN | Ling M.H., Wang C.G., Wang D.C., Chi C.W.; | | | | | | | |
| DN | Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases. | | | | | | | |
| DN | -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY); | | | | | | | |
| DN | !-!- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. | | | | | | | |
| DN | EMBL: AF064821; AAD31592.1; -. | | | | | | | |
| DR | HSSP: P01494; 2SN3. | | | | | | | |
| DR | InterPro: IPR003614. | | | | | | | |
| DR | InterPro: IPR002061; Scorpion_toxinI. | | | | | | | |
| DR | PFAM: PF00537; toxin_3; 1. | | | | | | | |
| DR | SMART: SM00505; Knot1; 1. | | | | | | | |
| KW | Neurotoxin; Signal. | | | | | | | |
| SIGNAL | 1 | 21 | POTENTIAL. | | | | | |
| CHAIN | 22 | 85 | NEUROTOXIN AEP. | | | | | |
| 3Q SEQUENCE | 85 AA: | 9312 MW: | CCE4671IBAF2DAC CRC64; | | | | | |
| Alignment Scores: | | | | | | | | |
| Refined No.: | 0.0783 | | Length: | 85 | | | | |
| Score: | 81.50 | | Matches: | 14 | | | | |
| Percent Similarity: | 55.26% | | Conservative: | 7 | | | | |
| Best Local Similarity: | 36.84% | | Mismatches: | 12 | | | | |
| Query Match: | 25.15% | | Indels: | 5 | | | | |
| DB: | 5 | | Gaps: | 2. | | | | |
| JS-09-673-274B-2 (1-169) × Q9XY87 (1-85) | | | | | | | | |
| Dy | 16 TCTGGCTGCTGGCTGCTGTGAAACTACATTCGATGCCAAGGGTAGTGCAGAGGAGG 75 | | | | | | | |
| Db | 34 Ser/Cys/Trp | | | | | | | |
| Dy | 76 GGTACAAAGGGTGCTCACTGGCTCTTCGTAACGTGAACGTGGCTGGAG 129 | | | | | | | |
| Db | 50 GlyAlaSerTyrGlyTyrCysTrpThrTrp--GlyLeuAlaCysTrpCysGln 66 | | | | | | | |
| RESULT 5 | | | | | | | | |
| D | Q9XY87 | | PRELIMINARY; | | PRT; | 85 AA. | | |
| AC | Q9XY87; | | | | | | | |
| DT | 01-NOV-1999 (TREMBLre). | 12. | Created | | | | | |
| DT | 01-NOV-1999 (TREMBLre). | 12. | Last sequence update | | | | | |
| DT | 01-MAR-2003 (TREMBLre). | 23. | Last annotation update | | | | | |
| DE | Neurotoxin | | | | | | | |
| DE | Scorpion | | | | | | | |
| DS | Mesobuthus martensii (Manchurian scorpion) | | | | | | | |
| DC | Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones; | | | | | | | |
| DC | Buthidae; Mesobuthus. | | | | | | | |
| NCBI_TaxID=14649; | | | | | | | | |
| DN | SEQUENCE FROM N.A. | | | | | | | |
| DN | Ling M.H., Wang C.G., Wang D.C., Chi C.W.; | | | | | | | |
| DN | Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases. | | | | | | | |
| DN | -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY); | | | | | | | |
| DN | !-!- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. | | | | | | | |
| DN | EMBL: AF064821; AAD31592.1; -. | | | | | | | |
| DR | HSSP: P01494; 2SN3. | | | | | | | |
| DR | InterPro: IPR003614. | | | | | | | |
| DR | InterPro: IPR002061; Scorpion_toxinI. | | | | | | | |
| DR | PFAM: PF00537; toxin_3; 1. | | | | | | | |
| DR | SMART: SM00505; Knot1; 1. | | | | | | | |
| KW | Neurotoxin; Signal. | | | | | | | |
| SIGNAL | 1 | 21 | POTENTIAL. | | | | | |
| CHAIN | 22 | 85 | NEUROTOXIN AEP. | | | | | |
| 3Q SEQUENCE | 85 AA: | 9312 MW: | CCE4671IBAF2DAC CRC64; | | | | | |
| Alignment Scores: | | | | | | | | |
| Refined No.: | 0.0783 | | Length: | 85 | | | | |
| Score: | 81.50 | | Matches: | 14 | | | | |
| Percent Similarity: | 55.26% | | Conservative: | 7 | | | | |
| Best Local Similarity: | 36.84% | | Mismatches: | 12 | | | | |
| Query Match: | 25.15% | | Indels: | 5 | | | | |
| DB: | 5 | | Gaps: | 2. | | | | |
| JS-09-673-274B-2 (1-169) × Q9XY87 (1-85) | | | | | | | | |
| Dy | 16 TCTGGCTGCTGGCTGCTGTGAAACTACATTCGATGCCAAGGGTAGTGCAGAGGAGG 75 | | | | | | | |
| Db | 34 Ser/Cys/Trp | | | | | | | |
| Dy | 76 GGTACAAAGGGTGCTCACTGGCTCTTCGTAACGTGAACGTGGCTGGAG 129 | | | | | | | |
| Db | 50 GlyAlaSerTyrGlyTyrCysTrpThrTrp--GlyLeuAlaCysTrpCysGln 66 | | | | | | | |
| RESULT 6 | | | | | | | | |
| P82761 | PRELIMINARY; | | PRT; | 9: | AA. | | | |
| AC | P82761; | | | | | | | |
| DT | 01-OCT-2002 (TREMBLre). | 22. | Created | | | | | |
| DT | 01-OCT-2002 (TREMBLre). | 22. | Last sequence update | | | | | |
| DT | 01-OCT-2002 (TREMBLre). | 22. | Last annotation update | | | | | |
| DE | Hypothetical protein LCR46 precursor. | | | | | | | |
| GN | LCR46. | | | | | | | |
| OS | Arabidopsis thaliana (Mouse-ear cress). | | | | | | | |
| OC | Vitidiplante; Streptophytina; Embryophyta; Tracheophyta; Rosidae; | | | | | | | |
| OC | Spermatophytina; Magnoliophyta; eudicots; core eudicots; Rosidae; | | | | | | | |
| OC | eurosidii II; Brassicales; Brassaceae; Arabidopsidales. | | | | | | | |
| RN | [1] | | | | | | | |
| RN | SEQUENCE FROM N.A. | | | | | | | |
| RC | STRAIN=cv. Co-umbria; | | | | | | | |
| RX | MEDLINE=9939451; PubMed=10470850; | | | | | | | |
| RA | Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H., Miyajima N., Tabata S., | | | | | | | |
| RT | "Structural analysis of Arabidopsis thaliana chromosome 5." X | | | | | | | |
| RT | Sequence features of the regions of 1,011,550 bp covered by seventeen TAC clones." | | | | | | | |
| RL | DNA Res. 6:183-195 (1999). | | | | | | | |
| RN | [2] | | | | | | | |
| RP | IDENTIFICATION | | | | | | | |
| RX | Pubmed=11437247; | | | | | | | |
| RA | Vanoosthuyse V., Miege C., Dumas C., Cock J.M.; | | | | | | | |
| RT | "Two large Arabidopsis thaliana gene families are homologous to the Brassica gene superfamily that encodes pollen coat proteins and the | | | | | | | |
| RT | Brassicaceae; Brassicales; Brassaceae; Arabidopsidales. | | | | | | | |
| ID | Q8T3T0 | | PRELIMINARY; | | PRT; | 85 AA. | | |

rate component of the self-incompatibility response."; Plant Mol. Biol. 46:17-34 (2001); EMBL: ABC17061; NOT_ANNOTATED_CDS; HYPOTHETICAL PROTEIN; Signal; SIGNAL 1 27 POTENTIAL HYPOTHETICAL PROTEIN LOC45647; CHAIN 28 91 MW: 19205.6; SEQUENCE 9: AA: 9503; MW: 19205.6; SEQUENCE 9: AA: 9503; MW: 19205.6;

| | | | | |
|------------------|--|---|------------------------|--|
| Qy | 34 |-CAGCACCCC 26 | DR | FlyBase; FBgn0031434; CG10812. |
| Db | 73 | PheserproteGlunisPro 79 | DR | InterPro; IPB002118; Gamma-thionin. |
| | | | DR | ProDom; PD02594; Gamma-thionin; 1. |
| RESULT :2 | | | SQ | SEQUENCE 69 AA; 7656 MW; 7255SFDB81DCC6F7 CRC64; |
| G9VZR2 | PRELIMINARY; | PRT; | Length: | 69 |
| ID | Q9VZR2 | | Matchs: | 15 |
| AC | | | Conservative: | 2 |
| DT | 01-MAY-2000 (TREMBL); 13; Last sequence update; | | Percent Similarity: | 42.50% |
| DT | 01-MAR-2003 (TREMBL); 23; Last annotation update) | | Best Local Similarity: | 37.50% |
| DE | CG10812 protein (GHD05576P); | | Query Match: | 22.99% |
| CN | CG10812 | | DB: | 5 |
| OS | Drosophila melanogaster (Fruit fly). | | DB: | 3 |
| OC | Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; | | | |
| OC | Neoptera; Endopterygota; Dipatra; Brachycera; Muscomorpha; | | | |
| OC | Ephydriidae; Drosophilidae; Drosophila. | | | |
| QX | NCBI TaxID=2227; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN:BERKELEY; | | | |
| RX | MECLINE=20196006; PubMed=10731132; | | | |
| RA | Adams M.D., Celiklar S.E., Holt R.A., Evans C.A., Gocayne J.D., | | | |
| RA | Amanatides P.G., Scheer S.E., Li P.W., Hoskins R.A., Galle R.F., | | | |
| RA | George R.A., Lewis S.E., Richards S., Henderson S.N., | | | |
| RA | Wortman J.B., Yandell M.D., Zhang Q., Chen L.X., | | | |
| RA | Branda R.C., Rogers Y.-H.C., Blaize, R.G., Champé M., Pfeiffer B.D., | | | |
| RA | Wat K.H., Dcyle C., Baxter E.G., Heit G., Nelson C.R., Miklos G.L.G., | | | |
| RA | Abrial J.F., Agbayani A., An H.-J., Andrews-Pfleiderer C., Baldwin D., | | | |
| RA | Bai J.W., Basu A., Baxendale J., Bayakatoglu L., Beasley S.M., | | | |
| RA | Beeson K.Y., Benos P.V., Boenigk D.P., Bozhakov S., | | | |
| RA | Borkova D., Botchan M.R., Buck C., Brodtier P., | | | |
| RA | Burtis K.C., Busam D.A., Butler H., Cadet E., Center A., Chandra I., | | | |
| RA | Cherry S., Dahirel C., Daverpon L.B., Dietz S.M., Dunn P., | | | |
| RA | de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Edgar-Rocha S., Dunkin P., | | | |
| RA | Dodson K., Doup L.E., Downes M., Edgar-Rocha S., Dunkin P., | | | |
| RA | Foster C., Gabrielian A.E., Ferreria S., Fleischmann W., | | | |
| RA | Godek A., Gong F., Gorrell J.H., Guan P., Harris M., Giasser K., | | | |
| RA | Harris J.M., Harvey D., Howland T.J., Herendeen J.R., Houck J., | | | |
| RA | Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ikegami C., | | | |
| RA | Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kerchukin K.A., | | | |
| RA | Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., | | | |
| RA | Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., | | | |
| RA | Liu X., Matrei B., McIntosh T.C., McLeod M.P., McPherson J., | | | |
| RA | Merkulov G., Milashina N.V., Mobley C., Morris J., Mosherf A., | | | |
| RA | Mount S.M., Moy M., Murphy L., Murry C.M., Nelson D.L., | | | |
| RA | Nelson D.R., Nelson K.A., Nixon K., Nusslein D.R., Pacieb J.M., | | | |
| RA | Pazzolo M., Pittman G.S., Pan S., Pardi J., Puri V., Reese M.G., | | | |
| RA | Reinert K., Remington K., Saunders R.D.C., Scheiffele F., Shen H., | | | |
| RA | Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., | | | |
| RA | Spirer E., Spradling A.C., Stapperton M., Strickland R., Sun E., | | | |
| RA | Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., | | | |
| RA | Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J., | | | |
| RA | Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., | | | |
| RA | Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zheng L., Zhai X., | | | |
| RA | Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Smith H.O., | | | |
| RA | Gibbs R.A., Myers E.W., Rubin G.M., Venet J.C., | | | |
| RC | "The genome sequence of Drosophila melanogaster." | | | |
| RC | Science 287:2185-2195(2000). | | | |
| RP | SEQUENCE FROM N.A. | | | |
| STRAIN:BERKELEY; | | | | |
| RA | Stapleton M., Brookstein B., Hong L., Agbayani A., Carlson J., | | | |
| RA | Champé M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., | | | |
| RA | George R., Gonzalez M., Guarin H., Krommler B., Li P., Liao G., | | | |
| RA | Miranda C.J., Mongalli C.J., Nunoo J., Parcels J., Park S., | | | |
| RA | Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., | | | |
| RA | Ceiniker S.; | | | |
| RA | Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases. | | | |
| RL | EMBL; AED03477; AAF47757.1; . | | | |
| DR | EMBL; AY118762; AAM50622.1; . | | | |
| DR | HSSP; P41964; IMN. . | | | |
| Qy | 19 | TGGTGTGGTGGTGGTGAACACTTCGAT----TGAAACGTGAGTGCAGAGG 72 | Length: | 84 |
| DB | 31 CysThrLeuAlaCysIleAspLysThrAspArgAspartateGCTGGTGCAGAG 50 | Matchs: | 14 | |
| Qy | 73 AGGGGTTACAGGGTGGTCACTGGTCTTCGCTAACGTGAACTGCTGGTGCAGAG 129 | Conservative: | 5 | |

b 51 GluGlyGlySerPheGlyHisCysSerTyrSerAla-----CysTrpCyslys 66

ESULT 14

D Q9GUAT7 PRELIMINARY; PRT; 85 AA.
 D Q9GUAT7_01-MAR-2001 (TREMBLrel. 16, Created)
 T 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 Hypothetical 9.4 kDa protein.
Mesobuthus martensii (Manchurian scorpion) (Buthus martensis)
Bukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones; Xiphosura; Mesobuthidae; Mesobuthus.
 NCBI_TaxID:34649;

[1] SEQUENCE FROM N.A.
 TISSUE=Venom gland;
 LI W.-X., Zeng X.-C., Zu S.-Y.;
 Submitted ('MAY-1999) to the EMBL/GenBank/DDBJ databases.
 -|- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).
 C C BELONGS TO: THE ALPHA/BETA-SCORPION TOXIN FAMILY
 EMBL: AF150009; AAG03657; 1; -.
 HSSP: P17728; ILQI.
 InterPro: IPR001614; Knot1.
 InterPro: IPR001219; Neurotoxin.
 InterPro: IPR003061; Scorpion_toxinL.
 Pfam: PF0037; toxin_3; 1.
 PRINTS: PRO0284; TOXIN.
 PRODOM: PDO00908; Scorpion_toxinL; 1.
 R R SMART: SM00505; Knot1; 1.
 Hypothetical protein.
 Q SEQUENCE 85 AA; 9426 MW; 6EFC43E02E95091 CRC64;

Alignment Scores:
 red. No.: 0.742 Length: 85
 core: 74.00 Matches: 12
 ercent Similarity: 64.29% Conservative: 6
 est Local Similarity: 42.86% Mismatches: 6
 b: b: 22.84% Indels: 4
 b: b: 5 Gaps: 2

S-09-673-274B-2 (1-169) × Q9GUAT7 (1-85)

red. No.: 0.742 Length: 85
 core: 74.00 Matches: 12
 ercent Similarity: 64.29% Conservative: 6
 est Local Similarity: 42.86% Mismatches: 6
 b: b: 22.84% Indels: 4
 b: b: 5 Gaps: 2

52 TGCAACGTGAGTGCAGAGGGTTACAAGGGTGTCACTGC-----GGTCTC 102
 D 41 CySpaspglucylslylslslylspgIAlaGluSerGlyTyrCysGlnTipAlaIyval 60
 T 01-MAR-2000 (TREMBLrel. 13, Created)
 T 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 E CG10813 Protein.

S Drosophila melanogaster (Fruit fly).

C Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

C Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

C Ephydriodea; Drosophilidae; Drosophila.

X X NCBI_TaxID:1227;

SEQUENCE FROM N.A.

C STRAIN:BERKELEY;

X MEDLINE:201906; PubMed=10731132;

A Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

A Amanatides P.G., Scheer S.E., Li P.W., Hoskins R.A., Galle R.F.,

A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Burton G.G., Wortman J.R., YangSeill M.D., Zhang Q., Chen L.X., Chen Y., Pleijffer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blaize R.G., Champé M., Miklos G.L.G.,

RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Baldwin J.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Bayraktaroglu L., Beasley E.M.,

RA Balow R.M., Basu S., Baxendale D., Bhandari D., Bolshakov S.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari P., Brodtier P.,

RA Botkova D., Botchan M.R., Bouc J., Brokstein P., Brottier P.,

RA Burris K.C., Busam D.A., Butler A., Cadieu E., Chandrasekharan, Center T.J., Davis P., Davis L.B., Dietz S.M.,

RA Cherry J.M., Cawley S., Datrice C., Davernport L., Deng Z., Mays A.D., Dew J.,

RA de Pablos B., Delcher A., Dietz S.M., Dugan-Rocha S., Dunn P.,

RA Dodson K., Douc L.E., Downs M., Dugan-Rocha S., Dunko J.C., Ferreria S., Fleischmann W.,

RA Durbin R.J., Evangelista C.C., Ferreria S., Gelbart W.M., Glasser K.,

RA Fosler C., Gabrielsson A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorreli J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Herman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Howland T.J., Ke M.-H., Liebman C.,

RA Jaijali M., Kalush F., Karper G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li Z., Lin X., Liang Y., Lin X.,

RA Liu X., Matrai B., Michtsoch T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milstina N.V., McBryde C., Morris J., Moskaleff A.,

RA Mount S.M., Murphy L., Murphy D.M., Neisler D.L.,

RA Nelson D.R., Nixon K.A., Nixon K.M., Nusslein D.R., Pacieb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Purif V., Reese X.G.,

RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spalding A.C., Stapleton M., Strong R., Sun E., Svartkas R., Tector C., Turner R., Venter C., Wang A.H., Wang X.,

RA Wang Z.-Y., Wasserman D.A., Werstrock G.M., Weissenbach J., Williams S.M., Woodage M., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang Q., Zhao Q., Zhou H.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., Venter J.C.,

RT "The genome sequence of *Drosophila melanogaster*";

RL Science 287:2185-2195(2000);

DR EMBL; AE03477; AAF47756; 1..

DR HSSP; PA1964; 1WYN.

DR FileBase; FBp005279; CG32279.

DR InterPro; IPR003614; Gamma-thionin.

DR InterPro; IPR003614; Knct1.

DR ProDom; PDO00594; Gamma-thionin; 1.

DR SMART; SMC0505; Knot1; 1.

DR Sequence 105 AA; 11598 MW; A76479C6E44BC50C CRR64;

DR SEQ

DR EMBL; AE03477; AAF47756; 1..

DR HSSP; PA1964; 1WYN.

DR FileBase; FBp005279; CG32279.

DR InterPro; IPR003614; Gamma-thionin.

DR ProDom; PDO00594; Gamma-thionin; 1.

DR SMART; SMC0505; Knot1; 1.

DR Sequence 105 AA; 11598 MW; A76479C6E44BC50C CRR64;

DR EMBL; AE03477; AAF47756; 1..

DR HSSP; PA1964; 1WYN.

DR FileBase; FBp005279; CG32279.

DR InterPro; IPR003614; Gamma-thionin.

DR ProDom; PDO00594; Gamma-thionin; 1.

DR SMART; SMC0505; Knot1; 1.

DR Sequence 105 AA; 11598 MW; A76479C6E44BC50C CRR64;

DR EMBL; AE03477; AAF47756; 1..

DR HSSP; PA1964; 1WYN.

DR FileBase; FBp005279; CG32279.

DR InterPro; IPR003614; Gamma-thionin.

DR ProDom; PDO00594; Gamma-thionin; 1.

DR SMART; SMC0505; Knot1; 1.

DR Sequence 105 AA; 11598 MW; A76479C6E44BC50C CRR64;

DR EMBL; AE03477; AAF47756; 1..

DR HSSP; PA1964; 1WYN.

DR FileBase; FBp005279; CG32279.

DR InterPro; IPR003614; Gamma-thionin.

DR ProDom; PDO00594; Gamma-thionin; 1.

DR SMART; SMC0505; Knot1; 1.

DR Sequence 105 AA; 11598 MW; A76479C6E44BC50C CRR64;

DR EMBL; AE03477; AAF47756; 1..

DR HSSP; PA1964; 1WYN.

DR FileBase; FBp005279; CG32279.

DR InterPro; IPR003614; Gamma-thionin.

DR ProDom; PDO00594; Gamma-thionin; 1.

DR SMART; SMC0505; Knot1; 1.

DR Sequence 105 AA; 11598 MW; A76479C6E44BC50C CRR64;

DR EMBL; AE03477; AAF47756; 1..

DR HSSP; PA1964; 1WYN.

DR FileBase; FBp005279; CG32279.

DR InterPro; IPR003614; Gamma-thionin.

DR ProDom; PDO00594; Gamma-thionin; 1.

DR SMART; SMC0505; Knot1; 1.

DR Sequence 105 AA; 11598 MW; A76479C6E44BC50C CRR64;

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DR InterPro; IPR003614; Gamma-thionin.

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DR SMART; SMC0505; Knot1; 1.

DR Sequence 105 AA; 11598 MW; A76479C6E44BC50C CRR64;

DR EMBL; AE03477; AAF47756; 1..

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DR FileBase; FBp005279; CG32279.

DR InterPro; IPR003614; Gamma-thionin.

DR ProDom; PDO00594; Gamma-thionin; 1.

DR SMART; SMC0505; Knot1; 1.

DR Sequence 105 AA; 11598 MW; A76479C6E44BC50C CRR64;

DR EMBL; AE03477; AAF47756; 1..

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DR ProDom; PDO00594; Gamma-thionin; 1.

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DR EMBL; AE03477; AAF47756; 1..

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DR FileBase; FBp005279; CG32279.

DR InterPro; IPR003614; Gamma-thionin.

DR ProDom; PDO00594; Gamma-thionin; 1.

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DR Sequence 105 AA; 11598 MW; A76479C6E44BC50C CRR64;

DR EMBL; AE03477; AAF47756; 1..

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DR FileBase; FBp005279; CG32279.

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DR Sequence 105 AA; 11598 MW; A76479C6E44BC50C CRR64;

DR EMBL; AE03477; AAF47756; 1..

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DR Sequence 105 AA; 11598 MW; A76479C6E44BC50C CRR64;

DR EMBL; AE03477; AAF47756; 1..

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DR FileBase; FBp005279; CG32279.

DR InterPro; IPR003614; Gamma-thionin.

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DR Sequence 105 AA; 11598 MW; A76479C6E44BC50C CRR64;

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DR FileBase; FBp005279; CG32279.

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DR Sequence 105 AA; 11598 MW; A76479C6E44BC50C CRR64;

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DR EMBL; AE03477; AAF47756; 1..

DR HSSP; PA1964; 1WYN.

DR FileBase; FBp005279; CG32279.

DR InterPro; IPR003614; Gamma-thionin.

DR ProDom; PDO00594; Gamma-thionin; 1.

DR SMART; SMC0505; Knot1; 1.

DR Sequence 105 AA; 11598 MW; A76479C6E44BC50C CRR64;

DR EMBL; AE03477; AAF47756; 1..

DR HSSP; PA1964; 1WYN.

DR FileBase; FBp005279; CG32279.

DR InterPro; IPR003614; Gamma-thionin.

DR ProDom; PDO00594; Gamma-thionin; 1.

DR SMART; SMC0505; Knot1; 1.

DR Sequence 105 AA; 11598 MW; A76479C6E44BC50C CRR64;

DR EMBL; AE03477; AAF47756; 1..

DR HSSP; PA1964; 1WYN.

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GenCore version 5.1.6

SUMMARIES

| | | Result No. | Score | Query Match length CB | ID | Description |
|---|--|------------|-------|-----------------------|----|-------------|
| DB nucleic - protein search, using frame_plus_n2p model | | 1 | 267 | 82.4 | 44 | AY54375 |
| run on: | October 16, 2003, 17:06:33 ; Search time 52.2159 Seconds | 2 | 267 | 82.4 | 44 | ABB76860 |
| (without alignments) | | 3 | 267 | 82.4 | 44 | ABB76868 |
| 1027.456 Million cell updates/sec | | 4 | 267 | 82.4 | 43 | AY54374 |
| title: | US-09-673-274B-2 | 5 | 267 | 82.4 | 74 | AY54376 |
| perfect score: | 324 | 6 | 266 | 82.1 | 44 | ABB76895 |
| sequence: | 1 gataaggcttacgtttccatg.....gaacgttgtcgacggatccgg 169 | 7 | 264 | 81.5 | 44 | ABB76863 |
| coring table: | BLOSUM62 | 8 | 264 | 81.5 | 44 | ABB76864 |
| Xgapext 10.0 Xgapext 0.5 | | 9 | 264 | 81.5 | 44 | ABB76872 |
| Ygapext 10.0 Ygapext 0.5 | | 10 | 264 | 81.5 | 23 | ABB76895 |
| Fgapext 6.0 Fgapext 7.0 | | 11 | 262 | 80.9 | 44 | ABB76862 |
| Delop 6.0 Delop 7.0 | | 12 | 262 | 80.9 | 44 | ABB76865 |
| Searched: | 1107863 seqs, 158726573 residues | 13 | 262 | 80.9 | 44 | ABB76867 |
| Total number of hits satisfying chosen parameters: | 2215726 | 14 | 262 | 80.9 | 44 | ABB76869 |
| Minimum DB seq length: 0 | | 15 | 262 | 80.9 | 44 | ABB76871 |
| Maximum DB seq length: 2000000000 | | 16 | 261 | 80.6 | 44 | ABB76866 |
| Post-processing: Minimum Match 0% | | 17 | 261 | 80.6 | 44 | ABB76870 |
| Maximum Match 100% | | 18 | 261 | 80.6 | 44 | ABB76894 |
| Listing first 45 summaries | | 19 | 259 | 75.9 | 44 | ABB76873 |
| | | 20 | 258 | 75.9 | 44 | ABB76898 |
| | | 21 | 256 | 79.0 | 44 | ABB76861 |
| | | 22 | 256 | 79.0 | 44 | ABB76897 |
| | | 23 | 255 | 78.7 | 44 | ABB76882 |
| | | 24 | 254 | 78.4 | 44 | ABB76874 |
| | | 25 | 254 | 78.4 | 44 | ABB76875 |
| | | 26 | 253 | 78.1 | 44 | ABB76879 |
| | | 27 | 253 | 78.1 | 44 | ABB76885 |
| Command line parameters: | | 28 | 251 | 77.5 | 23 | ABB76876 |
| MODEL-frame+ n2p model -DEV=xlp | | 29 | 251 | 77.5 | 44 | ABB76877 |
| Q= /cgn2_1/n2p/spoto spoto /US096732/4/runat 17062003 170626 2523/app_query.fasta_1_654 | | 30 | 251 | 77.5 | 44 | ABB76881 |
| -DB=A GenSeq 1\$run03 -QFMT=fastar -SUFFIX=rax -MNNMATCH=0.1 -LOOPCL=0 | | 31 | 251 | 77.5 | 44 | ABB76884 |
| -DB=B GenSeq 1\$run03 -QFMT=fastar -SUFFIX=rax -MNNMATCH=0.1 -LOOPCL=0 | | 32 | 251 | 77.5 | 44 | ABB76886 |
| -LIST=15 -DOCALIGNN=200 -START=1 -END=1 -TRANS=humanAC.cdi | | 33 | 250 | 77.2 | 44 | ABB76880 |
| -LIST=15 -DOCALIGNN=200 -START=1 -END=1 -TRANS=humanAC.cdi | | 34 | 250 | 77.2 | 23 | ABB76883 |
| MODE=LOCAL -OUTFILE=PO -NORMEXT=-HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 | | 35 | 248 | 76.5 | 44 | ABB76887 |
| USER=0 MRNP -NO MRNP -NORMEXT=0 -NORMALIZE=0 -WAIT=0 -NCPU=6 -ICPU=3 | | 36 | 248 | 76.5 | 44 | ABB76888 |
| -LARGEQUERY -NEG SCORE=0 -NEG SCORE=0 -WAIT=0 -DSBLOCK=100 -LONGLOG | | 37 | 246 | 75.9 | 44 | ABB76878 |
| DEV TIMEOUT=120 -WARN TIMEOUT=10 -XGAPEXT=0.5 -FGAPPOP=6 | | 38 | 246 | 75.9 | 44 | ABB76889 |
| FGAPEXT=7 -YGAPOP=10 -YGAPOP=10 -DELOP=6 -DELEXT=7 | | 39 | 246 | 75.9 | 44 | ABB76890 |
| Database : | A_Geneseq_19Jun03: * | 40 | 243 | 75.0 | 44 | ABB76892 |
| | /SIDSL/gcldata/geneseq/geneseqp-emb1/AA198C.DAT:* | 41 | 243 | 75.0 | 44 | ABB76899 |
| | /SIDSL/gcldata/geneseq/geneseqp-emb1/AA1981.DAT:* | 42 | 241 | 74.4 | 23 | ABB76891 |
| | /SIDSL/gcldata/geneseq/geneseqp-emb1/AA1982.DAT:* | 43 | 238 | 73.5 | 44 | ABB76893 |
| | /SIDSL/gcldata/geneseq/geneseqp-emb1/AA1983.DAT:* | 44 | 232 | 71.6 | 44 | ABP55988 |
| | /SIDSL/gcldata/geneseq/geneseqp-emb1/AA1984.DAT:* | 45 | 232 | 71.6 | 73 | ABP55987 |

ALIGNMENTS

RESULT 1

| | |
|---|---------------------------|
| ID AAY54375 | standard; Peptide; 44 AA. |
| XX | |
| XX | |
| AC AAY54375; | |
| XX | |
| DT 06-APR-2000 (first entry) | |
| XX | |
| DE Amino acid sequence of a heliomycin peptide. | |
| XX | |
| KW Heliomycin; polycysteine peptide; antifungal; antibacterial; | |
| XX | |
| KW Helicomyces infection; plant protection; animal protection; | |
| XX | |
| KW transgenic Plant; fungi; bacteria; Cercospora beticola; | |
| XX | |
| KW Cladosporium herbarum; Fusarium culmorum; F. oxysporum; | |
| XX | |
| KW Phytophthora cinnamomi. | |
| XX | |
| OS Heliothis virescens. | |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | | | | |
|--|--|---|---|---------------------|
| DA | (ENTO-) ENTOMED SA. | | | |
| CX | Dimarcq J, Legrain M, Menin L; | PR 15-APR-1998; 98FR-0C24933. | XX | |
| CX | | XX (RHON) RHONE POULENC AGRICHEMIE. | PA | |
| CX | | XX | DR 2000-108532/-0. | |
| CX | | XX N-PSDB; AA245631. | PT New polycysteine peptides, designated heliomycin, with antifungal or | |
| PT | New peptide derivatives of heliomycin, useful as antibacterial and | PT antibiotic agents in human or veterinary medicine and agriculture - | PT antibacterial activity, useful in medicine or plant protection. | |
| CX | | XX | PT | |
| CX | Claim 15; Page 57; 100pp; French. | PS Claim 13; Page 31; 46pp; French. | PS | |
| CX | The present invention relates to peptide derivatives of heliomycin with | CC The present sequence represents a fusion peptide of 5 amino acids | CC | |
| CX | antifungal and/or antibacterial activity. The present sequence is one | CC derived from the Mat alpha factor (MF-alpha) and heliomycin. The | CC | |
| CX | such peptide. The peptides are useful in human and veterinary medicine | CC attachment of the MF-alpha peptide sequence to the N-terminal aids secretion | CC | |
| CX | and in plant protection, for control of bacterial and fungal infections. | CC of the heliomycin peptide. Heliomycin is a polycysteine peptide with | CC | |
| CX | An antifungal and/or antibacterial composition containing at least one | CC antifungal and antibacterial activity, isolated from the lepidopteron | CC | |
| CX | peptide is also claimed. | CC Heliothis virescens. Heliomycin peptides contain the sequence given in | CC | |
| CX | | CC AAY54378. The heliomycin peptides are used as pharmaceuticals for | CC | |
| CX | Sequence 44 AA; | CC treating or preventing fungal infections in humans and animals. They | CC | |
| Alignment Scores: | | CC may also be used as antifungal agents for plant protection. Nucleic | CC | |
| Alignment No.: | 6.42e-26 | CC acid encoding the heliomycin peptides is used to generate transgenic | CC | |
| Score: | 267.00 | CC plants that are resistant to some fungi and bacteria (specifically | CC | |
| Percent Similarity: | 100.00% | CC Cercospora beticola, Cladosporium fulvum, Fusarium culmorum, | CC | |
| 38st Local Similarity: | 100.00% | CC F. oxysporum and Phytophthora cinnamomi), and for recombinant production | CC | |
| Query Match: | 82.41% | CC of the peptides. | CC | |
| DB: | 23 | XX Sequence 49 AA; | SO | |
| US-09-673-274B-2 (1-169) × ABB76868 (1-44) | | Alignment Scores: | 6.54e-26 | Length: 49 |
| Qy | 1 GATAAGCTTATCGCTTCTGGCTGCTGGGGTGAACTCAACTTCCGATTGCAAACGGT 60 | pred. No.: | 267.00 | Matches: 44 |
| Db | 1 AspLysLeuIleGlySerCysValTrpGlyAlaValAsnTrpThrSerAspCysAsnGly 20 | Score: | 0.00% | Conservative: 0 |
| Qy | 61 GAGTCAAGAGGGGGTTACAAGGGGTCACTGGTCACTGGTAACTGAACTGC 120 | Percent Similarity: | 100.00% | Mismatches: 0 |
| Db | 21 GlucosylsArgGlyTyrLysGlySerPheAlaAsnValAsnCys 40 | Best Local Similarity: | 100.00% | Indels: 0 |
| Qy | 121 TGGTGGCGGACT 132 | Query Match: | 82.41% | Gaps: 0 |
| Db | 41 TrpCysGluThr 44 | DB: 21 | | |
| RESULT 4 | | US-09-673-274B-2 (1-169) × AAY54374 (-49) | | |
| DA | AAY54374 standard; Peptide: 49 AA. | Qy 1 GATAMGCTTATCGCTTCTGGCTGCTGGGGTGAACTCAACTTCCGATTGCAAACGGT 60 | Qy 1 | Length: 49 |
| CX | | 6 AspLysLeuIleGlySerCysValTrpGlyAlaValAsnTrpThrSerAspCysAsnGly 20 | Db 6 | Matches: 44 |
| AC | AAY54374; | Qy 61 GAGTCAAGAGGGGGTTACAAGGGGTCACTGGTCACTGGTAACTGAACTGC 120 | Qy 61 | Conservative: 0 |
| CX | | Db 26 GlucosylsArgGlyTyrLysGlySerPheAlaAsnValAsnCys 40 | Qy 61 | Mismatches: 0 |
| DT | 06-APR-2000 (first entry) | Qy 121 TGGTGGCGGACT 132 | Db 121 | Indels: 0 |
| CX | Amino acid sequence of a fusion peptide of MF-alpha/heliomycin. | Qy 46 TrpCysGluThr 49 | Db 46 TrpCysGluThr 49 | Gaps: 0 |
| CX | Mat alpha factor; MF-alpha; heliomycin; polycysteine peptide; | RESULT 5 | | |
| CW | antifungal; antibacterial; fungal infection; plant protection; | AAY54376 | | |
| CW | animal protection; transgenic plant; fungi; bacteria; | ID AAY54376 standard; Peptide: 74 AA. | | |
| CW | Cercospora beticola; Cladosporium herbarum; Fusarium culmorum; | XX | | |
| CW | F. oxysporum; Phytophthora cinnamomi. | AC AAY54376; | | |
| CX | Chimeric - Saccharomyces cerevisiae. | XX | | |
| CX | Chimeric - Heliothis virescens. | DE A fusion peptide of PR-lalpha signal peptide/heliomycin. | | |
| Key | Location/Qualifiers | XX | | |
| H | 1..5 | KW PR-lalpha; heliomycin; polycysteine peptide; antifungal; antibacterial; | | |
| Peptide | /note= "residues derived from the yeast Mat-alpha | KW fungal infection; plant protection; animal protection; transgenic plant; | | |
| H | (MF-alpha) factor" | KW fungi; bacteria; Cercospora beticola; Cladosporium herbarum; | | |
| Peptide | 6..49 | KW Fusarium culmorum; F. oxysporum; Phytophthora cinnamomi. | | |
| H | /note= "heliomycin residues" | XX | | |
| CX | | OS Chimeric - Nicotiana sp. | | |
| CX | | OS Heliothis virescens. | | |
| CX | | XX | | |
| 2D | 22-OCT-1999. | PH Key | | Location/Qualifiers |
| CX | | FT Peptide 1..30 | | |
| 2F | 15-APR-1998; 98FR-0004933. | FT /note= "tobacco PR-lalpha signal peptide" | | |

Pag 4

| | | |
|---|------------------------------------|---|
| X | 05-JUL-2001; 2001WO-FR02164. | PA (ENTC-) ENTOMED SA. |
| X | 13-JUL-2000; 2000FR-0009248. | XX Dimarcq J., Legrain M., Menin L; |
| R | 19-SEP-2000; 2000FR-0011949. | XX DR WPI; 2002-179779/23. |
| X | (ENTO-) ENTOMED SA. | XX New peptide derivatives of heliomicine, useful as antibacterial and antifungal agents in human or veterinary medicine and agriculture. |
| X | I Dimarcq J., Legrain M., Menin L; | XX PT Claim 15; Page 57; 100pp; French. |
| X | X | XX The present invention relates to peptide derivatives of heliomicine with antifungal and/or antibacterial activity. The present sequence is one such peptide. The peptides are useful in human and veterinary medicine and in plant protection, for control of bacterial and fungal infections. An antifungal and/or antibacterial composition containing at least one peptide is also claimed. |
| X | X | XX Sequence 44 AA; |
| X | X | Alignment Scores: |
| X | X | Pred. No.: 1.57e-25 Length: 44 |
| X | X | Score: 264.00 Matches: 43 |
| X | X | Percent Similarity: 100.00% Conservative: 1 |
| X | X | Best Local Similarity: 97.73% Mismatches: 0 |
| X | X | Query Match: 81.48% Indels: 0 |
| X | X | DB: 23 Gaps: 0 |
| X | X | US-09-673-274B-2 (1-169) x ABB76864 (1-44) |
| X | X | QY 1 GATAAGCTTATGGTTATGGGCTGTGAACACTTCGATTGCAACGGT 60 |
| X | X | Db 1 AspLysLeuIleGlySerCysValTrpGlyAlaValAsnTyThrThrAspCysAsnCys 20 |
| X | X | QY 61 GAGTGCAAGAGGGTTACAGGGTCTCGGTGCTGGTGAACCTCCGTTGCTAACGTGAACCTC 120 |
| X | X | Db 21 GlucysLysArgArgGlyTyrrylsGlyHisCysGlySerPheAaaValAsnCys 40 |
| X | X | QY 62 GAGTGCAAGAGGGGTTACAGGGTGTCACTGGGTCCTCGCTAACGTGAACCTC 132 |
| X | X | Db 4: TrpCysGluThr 44 |
| X | X | RESULT 9 ABB76872 |
| X | X | ID ABB76872 standard; Protein: 44 AA. |
| X | X | XX AC ABB76872; |
| X | X | XX DT 03-JUL-2002 (first entry) |
| X | X | DE Artifungal/antibacterial peptide pEX1. |
| X | X | XX KW Antifungal; antibacteria; fungicide; heliomicine; human medicine; |
| X | X | KW veterinary medicine; plant protection; bacterial infection; |
| X | X | KW fungal infection. |
| X | X | OS Synthetic. |
| X | X | XX PN WO200206324-A2. |
| X | X | XX PR 13-JUL-2000; 2000CFR-0C39248. |
| X | X | PR 19-SEP-2000; 2000FR-0011949. |
| X | X | XX PA (ENTO-) ENTOMED SA. |
| X | X | XX P1 Dimarcq J., Legrain M., Menin L; |
| X | X | XX DR WPI; 2002-179779/23. |
| b | Y | RESULT 8 BB76864 D ABB76864 standard; Protein: 44 AA. |
| b | Y | XX ABB76864; 03-JUL-2002 (first entry) |
| b | Y | XX DE Antifungal/antibacterial peptide pEM43. |
| b | Y | XX KW Antifungal; antibacterial; fungicide; heliomicine; human medicine; |
| b | Y | KW veterinary medicine; plant protection; bacterial infection; |
| b | Y | KW fungal infection. |
| b | Y | Synthetic. |
| b | Y | XX WO200206324-A2. |
| b | Y | XX PR 24-JAN-2002. |
| b | Y | XX XX 05-JUL-2001; 2001WO-FR02164. |
| b | Y | XX XX 13-JUL-2000; 2000CFR-0C39248. |
| b | Y | XX XX 19-SEP-2000; 2000FR-0011949. |
| b | Y | XX PA (ENTO-) ENTOMED SA. |
| b | Y | XX P1 Dimarcq J., Legrain M., Menin L; |
| b | Y | XX DR WPI; 2002-179779/23. |

| | | | |
|---|--|---|-----|
| Db | 21 | GlucyslysArgGlyTyrLysGlyGlyHisCysGlySerPheLeuAsnValAsnCys | 40 |
| Qy | 121 | TGGTGGAGACT | 132 |
| Db | 41 | TpcysGluThr | 44 |
| RESULT 15 | | | |
| | ABB76871 | standard; Protein: 44 AA. | |
| XX | XX | DT 03-JUL-2002 (first entry) | |
| DE | Antifungal/antibacterial peptide pEM7. | | |
| XX | Antifungal; antibacterial; fungicide; heliomicine; human medicine; | | |
| KW | veterinary medicine; plant protection; bacterial infection; | | |
| KW | fungal infection. | | |
| XX | Synthetic. | | |
| OS | | | |
| XX | WO200206324-A2. | | |
| PK | PD 24-JAN-2002. | | |
| XX | PF 05-JUL-2001; 2CC1WO-PR02164. | | |
| XX | PR 13-JUL-2000; 2000FR-0009248. | | |
| PR 19-SEP-2000; 2000FR-001949. | | | |
| XX | (ENTC-) ENTOMED SA. | | |
| PA | Dimarcq J, Legrain M, Menin L; | | |
| XX | DR WPI; 2002-179779/23. | | |
| PT New peptide derivatives of heliomicine, useful as antibacterial and | | | |
| PR antifungal agents in human or veterinary medicine and agriculture - | | | |
| XX | PS Claim : 5; Page 57; 100pp; French. | | |
| XX | The present invention relates to peptide derivatives of heliomicine with | | |
| CC antifungal and/or antibacterial activity. The present sequence is one | | | |
| CC such peptide. The peptides are useful in human and veterinary medicine | | | |
| CC and in plant protection, for control of bacterial and fungal infections. | | | |
| CC An antibacterial and/or antifungal composition containing at least one | | | |
| CC peptide is also claimed. | | | |
| XX | SQ Sequence 44 AA; | | |
| | Alignment Scores: | | |
| Aligned. No. : | 2.84e-25 | Length: | 44 |
| Score: | 262.00 | Matches: | 43 |
| Percent Similarity: | 100.00% | Conservative: | 0 |
| Best Local Similarity: | 100.00% | Mismatches: | 0 |
| Query Match: | 80.86% | Indels: | 0 |
| DB: | 23. | Gaps: | 0 |
| US-09-671-274B-2 (1-169) x ABB76871 (1-44) | | | |
| Qy | 1 GATAGCTATCGGTCTGGTGGTGCGGTGAACTACCTCCGATTGCAACGGT | 60 | |
| Db | 1 AspTleuIleGlySerCysValTyrGlyAlaValAsnTyrThrSerAspCysAlaGly | 20 | |
| Qy | 61 GAGTCAAAGGAGGGTTAACAGGTGTCACTCCGGTCTCTAACGTGAATCTGC | 120 | |
| Db | 21 GluysLysArgGlyTyrLysGlyGlyHisCysGlySerPheLeuAsnValAsnCys | 40 | |
| Qy | 121 TGGTGGAG 129 | | |
| Db | 41 TpcysGlu 43 | | |

search completed: October 16, 2003, 17:10:35
job time : 52.2159 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2003 Compugete Ltd.

DBM nucleic - protein search, using frame_plus_n2p model

run on: October 16, 2003, 17:12:07 ; Search time 35.094 Seconds
 (without alignments)
 1578.850 Million cell updates/sec

Title: US-09-673-274B-2

Effect score: 324
 Sequence: 1 gataaqtatcggttcctg.....gaaagtgtcgacggatccgg 169

coring table: BLASTM62
 Xgapext 10.0 , Xgapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 609560 seqs, 163917102 residues

Total number of bits satisfying chosen parameters: 1219120

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Command line parameters:

```
MODEL=frame+ n2p.model -DEV=xlp
Q=/csm2/1/USPro/spool/US967324/runat_16102003_170630_274/app/query.fasta_1.654
DB=Published Applications AA -QFMT=fafasean -SUFFIX=rapb -MINMATCH=0.1
LOOPCL=0 -IOGAPEXT=1 -UNITS=b16 -START=1 -END=1 -MATRIX=biocns62
TRANS-human40.cdi -LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100
THR MIN=0 -ALIGN=1 -MODE=LOCAL -OUTFMT pto -NORMEXT -HEAESTZE=500 -MINLEN=0
MAXFL=2000000000 -USER=16102003_170630_2743
NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORE=0 -WAIT=1
LONGLOG -DEV TIMEOUT=120 -WARN TIMEOUT=0 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
```

Published Applications AA: *

```
1: /cgn2_6/ptodata/2/pubpaas/PCT_NUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaas/PCT_NUBCOMB.pep:*
3: /cgn2_6/ptodata/2/pubpaas/US06_NUBCOMB.pep:*
4: /cgn2_6/ptodata/2/pubpaas/US06_NUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaas/US07_NUBCOMB.pep:*
6: /cgn2_6/ptodata/2/pubpaas/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaas/US08_NUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaas/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaas/US09_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaas/US09C_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaas/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaas/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaas/US10_NUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaas/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaas/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaas/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/2/pubpaas/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaas/US60_PUBCOMB.pep:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Match Length | DB ID | Description |
|------------|-------|-------|--------------|-------|-------------|
|------------|-------|-------|--------------|-------|-------------|

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1: 232 71.6 US-10-125-258-119
2: 232 71.6 US-10-125-258-117
3: 79.5 24.5 US-10-264-48C-13
4: 79.5 24.5 US-10-264-48C-11
5: 76.5 23.6 US-10-264-48C-9
6: 75 23.1 US-29-623-481-2
7: 74.5 23.0 US-10-180-247-4
8: 74.5 23.0 US-10-180-247-6
9: 74.5 23.0 US-10-180-247-2
10: 71.5 22.1 US-10-264-48C-6
11: 71.5 22.1 US-10-264-48C-7
12: 71.5 22.1 US-10-264-48C-8
13: 71 21.9 US-10-178-213-411
14: 71 21.9 US-10-178-213-410
15: 70.5 21.8 US-10-178-213-387
16: 70.5 21.8 US-10-264-48C-14
17: 70.5 21.8 US-10-178-213-386
18: 70.5 21.8 US-10-264-48C-10
19: 69.5 21.5 US-10-264-48C-18
20: 69 21.3 US-10-178-213-408
21: 69 21.3 US-10-178-213-444
22: 69 21.3 US-10-178-213-407
23: 69 21.3 US-10-178-213-443
24: 68.5 22.6 US-10-156-76-7787
25: 68 21.0 US-10-178-213-396
26: 68 21.0 US-10-178-213-395
27: 67.5 20.8 US-10-264-48C-12
28: 67.5 22.3 US-10-178-213-208
29: 67 20.7 US-10-178-213-168
30: 67 20.7 US-10-178-213-167
31: 67 20.7 US-10-178-213-22
32: 67 20.7 US-10-264-48C-23
33: 66.5 20.5 US-10-178-213-309
34: 66.5 20.5 US-10-178-213-319
35: 66.5 20.5 US-10-264-48C-4
36: 66.5 20.5 US-10-178-213-359-21
37: 66.5 20.5 US-10-264-48C-15
38: 66.5 20.5 US-10-178-213-308
39: 66.5 20.5 US-10-178-213-338
40: 66.5 21.9 US-10-156-76-10081
41: 66 21.8 US-09-764-868-677
42: 66 21.8 US-09-764-868-1100
43: 66 21.8 US-09-925-302-783
44: 65.5 20.2 US-10-178-213-147
45: 65.5 20.2 US-10-264-48C-3
```

ALIGNMENTS

```
RESULT 1
US-10-125-258-119
/ Sequence 119, Application US/10125258
/ Publication No. US20010C2892CA1
/ GENERAL INFORMATION:
/ APPLICANT: Altier, Daniel J.
/ APPLICANT: Herrmann, Rafael
/ APPLICANT: Iu, Albert J.
/ APPLICANT: McCutchen, Billy F.
/ APPLICANT: Presnail, James K.
/ APPLICANT: Weaver, Janine L.
/ APPLICANT: Wong, James F. H.
/ TITLE OF INVENTION: Antimicrobial Polypeptides and Their
```

```
/ TITLE OF INVENTION: Uses
```

```
/ FILE REFERENCE: 35718/246215
```

```
/ CURRENT APPLICATION NUMBER: US/10-125-258
```

```
/ CURRENT FILING DATE: 2002-04-18
```

```
/ PRIOR APPLICATION NUMBER: 60/785,355
```

```
/ PRIORITY FILING DATE: 2001-04-20
```

```
/ NUMBER OF SEQ ID NOS: 127
```

```
/ SOFTWARE: FastSEQ for Windows Version 4.0
```

```
/ LENGTH: 44
```

```
/ TYPE: PRT
```

ORGANISM: *Agrotis ipsilon*
US-10-125-258 1:9

RESULT 3
US-10-264-480-13
Sequence 13, Application US10264480
Publication No. US2003013892A1
GENERAL INFORMATION
APPLICANT: Hammock, Bruce D.
TITLE OF INVENTION: ISOLATED POLYPEPTIDES AND COMPOSITIONS FROM THE VENOM OF *P. TRANSVALICUS* AND METHODS OF USE
FILE REFERENCE: UCA-256
CURRENT APPLICATION NUMBER: US10/264,480
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: 60/393,370
PRIOR FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: 60/327,602
PRIOR FILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 13
LENGTH: 65
TYPE: PRT
ORGANISM: *Centruroides sculpturatus*
US-10-264-480-13

Alignment Scores:
Pred. No.: 0.34e-2:
Score: 232.00
Percent Similarity: 93.02%
Best Local Similarity: 88.37%
Query Match: 71.60%
DB: 15

Length: 44
Matches: 38
Conservative: 2
Mismatches: 3
Indels: 0
Gaps: 0

US-09-673-274B-2 (1:169) × US-10-125-258-1:9 (1:44)

Qy 1 GATAAGCTTATGGTTCTGGGTGGGTTGAACTCCATTGCCAACGGT 60
Lc 1 AspValHsLysGlySerCysValPrglyAlaValAspTyThrSerAsnCysAsnAsn 20

Qy 61 GAGTGCAGAGGAGGGGTACAAAGGTGGTACTCGGGTCTCGTAACGTGAACGTG 120
Db 21 CysCysLysArgArgGlyTyrLysGlyLysGlySerPheAlaAsnAsnCys 40

Qy :21 TGGTGGCAG 129
Dt 4: TrpCysGlu 43

Length: 65
Matches: 65
Conservative: 17
Best Local Similarity: 51.28%
Query Match: 43.59%
DB: 15

Alignment Scores:
Pred. No.: 0.162
Score: 79.50
Percent Similarity: 51.28%
Best Local Similarity: 43.59%
Query Match: 24.54%
DB: 15
LENGTH: 65

US-09-673-274B-2 (1:169) × US-10-264-480-13 (1:65)

Qy 19 TGGGTGGGGCTGCTGAACTACACTCCGATGTCAAACGGTGAGTCAGAGGGGT 78
Db 16 CyPhePheLeuDlyLysAsn----GluHisCysAsnThrGluCysLysAlaLysAsn 33

Qy 79 TRAAGGGT----GGTCACTGGG.TCCCTCGCTAACCTGAACTGCTGCTGCGAG 129
Db 34 GingLyGlySerTygTyrcystyFalaPheAla-----CystTrpCysGlu 49

RESULT 4
US-10-264-480-11
Sequence 11, Application US10/264480
Publication No. US2003013892A1
GENERAL INFORMATION
APPLICANT: Hammock, Bruce D.
TITLE OF INVENTION: ISOLATED POLYPEPTIDES AND COMPOSITIONS FROM THE VENOM OF *P. TRANSVALICUS* AND METHODS OF USE
FILE REFERENCE: UCA-256
CURRENT APPLICATION NUMBER: US10/264,480
CURRENT FILING DATE: 2002-10-04
PRIOR APPLICATION NUMBER: 60/393,070
PRIOR FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: 60/327,602
PRIOR FILING DATE: 2001-10-04
NUMBER OF SEQ ID NOS: 30A
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 11

Length: 66
Matches: 66
Conservative: 17
Best Local Similarity: 53.85%
Query Match: 24.54%

ORGANISM: *Agrotis ipsilon*
US-10-125-258 11:7

Alignment Scores:
Pred. No.: 8.94e-21
Score: 23.00
Percent Similarity: 93.02%
Best Local Similarity: 88.37%
Query Match: 71.60%
DB: 15

Length: 73
Matches: 38
Conservative: 2
Mismatches: 3
Indels: 0
Gaps: 0

US-09-673-274B-2 (1:169) × US-10-125-258 11:7 (1:73)

Qy 1 GATAAGCTTATGGTTCTGGGTGGGTTGAACTCCATTGCCAACGGT 60
Lc 1 AspValHsLysGlySerCysValPrglyAlaAspTyThrSerAsnCysAsn 49

Qy 61 GAGTGCAGAGGAGGGTACAAAGGTGGTACTCGGGTCTGAACTGCAACTG 120
Db 50 GluCysLysArgArgGlyTyrLysGlyLysCysGlySerPheAlaAsnCys 69

Qy :21 TGGTGCAG 129
Db 70 TrpCysGlu 72

Length: 66
Matches: 66
Conservative: 4
Best Local Similarity: 43.59%
Query Match: 24.54%

B: 15 Gaps: 3

JS-09-673-274B-2 (1-169) x US-10-264-480-11 (1-66)

Organism: Scolependra canadiens DS
US-09-829-481-2

Alignment Scores:
 Pred. No.: 0.594 Length: 61
 Score: 75.00 Matches: 11
 Percent Similarity: 53.57% Conservative: 4
 Best Local Similarity: 39.29% Mismatches: 13
 Query Match: 23.15% Indels: 0
 DB: 9 Gaps: 0

US-C9-673-274B-2 (1-169) x US-09-829-481-2 (1-61);

Qy 49 GATTGAAACGTTGACTGCAAGGAGGGTACAGGGGGTCACTGGTCCCTGGCT : 06
 Db 34 GluCysPheArgHs:sysA9GlyAsnGlyPheThrGlyGlyTyrCysGlyPhelHs : 51

Qy 109 AACGTGAACTGCTGTTGACTGACT : 132
 Db 54 LysPheThrCysLysCysTyrThr : 41

RESULT 7

JS-10-180-247-4
 Sequence 4 Application 15/1018247
 Publication No. US20030113892A1
 GENERAL INFORMATION:
 APPLICANT: Hammock, Bruce D.
 APPLICANT: Incegiu, Bora
 TITLE OF INVENTION: ISOLATED POLYPEPTIDES AND COMPOSITIONS FROM THE VENOM OF P. TRANSVAALICUS AND METHODS OF USE
 FILE REFERENCE: UCAL256
 CURRENT FILING NUMBER: US/10/264,480
 PRIORITY NUMBER: 60/393,070
 PRIOR FILING DATE: 2002-06-28
 PRIORITY NUMBER: 60/327,602
 PRIOR FILING DATE: 2001-10-04
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 9 LENGTH: 61
 TYPE: PRT
 ORGANISM: Leurus quinquestratus quinquestratus
 JS-10-264-480-9

Alignment Scores:
 Pred. No.: 0.384 Length: 61
 Score: 76.50 Matches: 15
 Percent Similarity: 55.26% Conservative: 6
 Best Local Similarity: 39.47% Mismatches: 12
 Query Match: 23.61% Indels: 5
 DB: 15 Gaps: 2

US-09-673-274B-2 (1-169) x US-10-264-480-9 (1-61)

Qy 16 TCTGGTGTGGGTGCTACTGGCTCCCTCGTAACCTTGCGTGTGAAGGGAGG 75
 Db 13 SerCysLeuPheGly-----AsnGlyCysAsnLysGluCysLysSerTyr 28

Qy 76 GTTACAGGGTGTGCTACTGGCTCCCTCGTAACCTTGCGTGTGAAGGGAGG 129
 Db 29 GlyGlySerTyrCysTrpThrTyr--GlyLeuAlaCysTrpCysGlu 45

US-09-829-481-2

Sequence 2, Application US/09829481
 Patent No. US20020059427A1
 GENERAL INFORMATION:
 APPLICANT: Presnail, James B.
 APPLICANT: Wong, Zude
 APPLICANT: Wong, James
 TITLE OF INVENTION: Arthropod Defensins
 FILE REFERENCE: B71441 US NA
 CURRENT APPLICATION NUMBER: US/09/829,481
 CURRENT FILING DATE: 2001-04-10
 PRIOR APPLICATION NUMBER: 60/197279
 PRIOR FILING DATE: 2000-04-14
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: Microsoft Office 97
 SEQ ID NO: 2 LENGTH: 61
 TYPE: PRT

RESULT 8

US-10-180-247-6
 Sequence 6 Application US/10180247
 Publication No. US20030113892A1

Qy 13 CGTTCTGC--GTGCGGTTGCTGTGACTACATGCCATTGAACTGGTCACTGCAAG 69
 Db 9 GlyProCysAlaValIrrAsp-----AsnGluThrCysArgValCysLys 24
 Qy 70 AGGGGGTACAAGGTTGGTCACTGGTCCCTTGCTAACGTGAACCTGGTGGAG : 29
 Db 25 GluGluGlyArgSerGlyHscysSer-----ProSerLeuLysCysTrpCysGlu 42

GENERAL INFORMATION:

APPLICANT: DeRose, Richard

APPLICANT: Freyinnet, Georges

TITLE OF INVENTION: Chimeric Gene Encoding Drosomycin, Vector Containing It and Production of Disease-Resistant Transgenic Plants

FILE REFERENCE: A32899-PCT-USA-A 072667 0:62

CURRENT APPLICATION NUMBER: US10/180,247

CURRENT FILING DATE: 2002-06-26

PRIOR APPLICATION NUMBER: PCT/FR98/01462

PRIOR FILING DATE: 1998-07-08

PRIOR APPLICATION NUMBER: FR97/09,115

PRIOR FILING DATE: 1997-C7-11

PRIOR APPLICATION NUMBER: FR97/09,663

PRIOR FILING DATE: 1997-07-24

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version: 4.0

SEQ ID NO: 6

LENGTH: 69

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Ubiquitin drosomycin fusion peptide

US 10/180,247-6

Alignment Scores:

| Pred. No.: | Length: | Score: | Percent Similarity: | Best Local Similarity: | Query Match: | DB: |
|------------|---------|--------|---------------------|------------------------|--------------|---|
| 0.699 | 69 | 74.50 | 42.5% | 37.50% | 22.99% | DB: |
| | | | | | | US-09-673-274B-2 (1-169) × US-10-180-247-2 (1-69) |
| | | | | | | US-09-673-274B-2 (1-169) × US-10-180-247-2 (1-70) |
| | | | | | | US-10-264-480-6 |
| | | | | | | Sequence 6, Application US/10264480 |
| | | | | | | Publication No. US2003013892A1 |
| | | | | | | GENERAL INFORMATION: |
| | | | | | | APPLICANT: Hammock, Bruce D. |
| | | | | | | APPLICANT: Ineoglu, Bora |
| | | | | | | TITLE OF INVENTION: ISOLATED POLYPEPTIDES AND COMPOSITIONS FROM THE VENOM OF P. TRANSVALICUS AND METHODS OF USE |
| | | | | | | FILE REFERENCE: JCAL256 |
| | | | | | | CURRENT APPLICATION NUMBER: US/10/264,480 |
| | | | | | | CURRENT FILING DATE: 2002-10-04 |
| | | | | | | PRIOR APPLICATION NUMBER: 60/393,370 |
| | | | | | | PRIOR FILING DATE: 2002-06-28 |
| | | | | | | PRIOR APPLICATION NUMBER: 60/327,602 |
| | | | | | | PRIOR FILING DATE: 2001-10-04 |
| | | | | | | NUMBER OF SEQ ID NOS: 30 |
| | | | | | | SOFTWARE: FastSEQ for Windows Version 4.0 |
| | | | | | | SEQ ID NO: 6 |
| | | | | | | LENGTH: 61 |
| | | | | | | TYPE: PRT |
| | | | | | | ORGANISM: Butracus arenicola |
| | | | | | | US-10-264-480-6 |
| | | | | | | Alignment Scores: |
| | | | | | | Pred. No.: |
| | | | | | | Score: |
| | | | | | | Percent Similarity: |
| | | | | | | Best Local Similarity: |
| | | | | | | Query Match: |
| | | | | | | DB: |
| | | | | | | US-09-673-274B-2 (1-169) × US-10-264-480-6 (1-61) |
| | | | | | | US-10-264-480-7 |
| | | | | | | Sequence 7, Application US/10264480 |
| | | | | | | Publication No. US2003013892A1 |
| | | | | | | GENERAL INFORMATION: |
| | | | | | | APPLICANT: Hammock, Bruce D. |
| | | | | | | APPLICANT: Ineoglu, Bora |
| | | | | | | TITLE OF INVENTION: ISOLATED POLYPEPTIDES AND COMPOSITIONS FROM THE VENOM OF P. TRANSVALICUS AND METHODS OF USE |
| | | | | | | FILE REFERENCE: UCAL256 |

RESULT 9

US-10-180-247-2

Sequence 2, Application US/10180247

Publication No. US2003016751A1

GENERAL INFORMATION:

APPLICANT: DeRose, Richard

APPLICANT: Hammock, Jules

TITLE OF INVENTION: Chimeric Gene Encoding Drosomycin, Vector Containing It and Production of Disease-Resistant Transgenic Plants

FILE REFERENCE: A32899-PCT-USA-A 072667 3182

CURRENT APPLICATION NUMBER: US10/180,247

CURRENT FILING DATE: 2002-06-26

PRIOR APPLICATION NUMBER: 09/480,251

PRIOR FILING DATE: 2000-01-11

PRIOR APPLICATION NUMBER: PCT/FR98/01462

PRIOR FILING DATE: 1998-07-08

PRIOR APPLICATION NUMBER: FR97/09,115

PRIOR FILING DATE: 1997-07-11

PRIOR APPLICATION NUMBER: FR97/09,663

NUMBER OF SEQ ID NOS: 15

SEQ ID NO: 2

LENGTH: 70

TYPE: PRT

CURRENT APPLICATION NUMBER: US/10/264,480
 CURRENT FILING DATE: 2002-10-04
 PRIOR APPLICATION NUMBER: 60/393,070
 PRIORITY FILING DATE: 2002-06-28
 PRIOR APPLICATION NUMBER: 60/327,602
 PRIORITY FILING DATE: 2001-10-04
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 7
 LENGTH: 61
 TYPE: PRT
 ORGANISM: *Butthus occitanus*
 JS-10-264-480-7

Alignment Scores:
 Pred. No.: 1.65 Length: 61
 Score: 71.50 Matches: 14
 Percent Similarity: 55.68 Conservate: 7
 Best Local Similarity: 36.94 Mismatches: 12
 Query Match: 15 Indels: 5
 DB: 2 Gaps: 2

JS-09-673-274B-2 (1-169) × US-10-264-480-7 (1-61)

Y 16 TCCCTCGTGGGGTGTGAACTACACTCCGATTGCAACGGTGACTGCCAGAGGAGG 75
 Y 13 SerCysLeuPheGly-----AsnGluCysCysAspLysAlaTyr 28

Db 76 GGTACAGGGTGGTCACTGGTTCCCTGCTAACGTGACTGCTGTCGAGCAG 129
 Db 29 GlyGlySertyrGlyTyrCysTrpThrTrp---GlyLeuAlaCysTrpCysGlu 45

RESULT 12
 JS-10-264-480-8
 , Sequence 8, Application US/10264480
 , Publication No. US20030113692A1
 , GENERAL INFORMATION:
 , APPLICANT: Hammock, Bruce D.
 , APPLICANT: Inceoglu, Bora
 , TITLE OF INVENTION: ISOLATED POLYPEPTIDES AND COMPOSITIONS FROM THE VENOM OF *P. TRANSVAALICUS* AND METHODS OF USE
 , FILE REFERENCE: UCAL256
 , CURRENT APPLICATION NUMBER: US/10/264,480
 , CURRENT FILING DATE: 2002-10-04
 , PRIOR APPLICATION NUMBER: 60/393,070
 , PRIORITY FILING DATE: 2002-06-28
 , PRIOR APPLICATION NUMBER: 60/327,602
 , PRIORITY FILING DATE: 2001-10-04
 , NUMBER OF SEQ ID NOS: 30
 , SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 8
 LENGTH: 61
 TYPE: PRT
 ORGANISM: *Butthus occitanus*
 JS-10-264-480-8

Alignment Scores:
 Pred. No.: 1.65 Length: 61
 Score: 71.50 Matches: 14
 Percent Similarity: 55.26 Conservate: 7
 Best Local Similarity: 36.84 Mismatches: 12
 Query Match: 22.07 Indels: 5
 DB: 15 Gaps: 2

US-09-673-274B-2 (1-169) × US-10-264-480-8 (1-61)

Y 16 TCCCTCGTGGGGTGTGAACTACACTCCGATTGCAACGGTGACTGCCAGAGGAGG 75
 Y 13 SerCysLeuPheGly-----AsnGluCysCysAspLysAlaTyr 28

Db 76 GGTACAGGGTGGTCACTGGTTCCCTGCTAACGTGACTGCTGTCGAGCAG 129
 Db 29 GlyGlySertyrGlyTyrCysTrpThrTrp---GlyLeuAlaCysTrpCysGlu 45

RESULT 13
 US-10-178-213-411
 , Sequence 411, Application US/10178213
 , Publication No. US2003041348A1
 , GENERAL INFORMATION:
 , APPLICANT: Simmons, Carl R.
 , APPLICANT: Navarro Acevedo, Pedro A.
 , APPLICANT: Harvell, Leslie
 , APPLICANT: Cahoon, Rebecca
 , APPLICANT: McCuchen, Billy Fred
 , APPLICANT: Lu, Albert
 , APPLICANT: Herrmann, Rafael
 , APPLICANT: Wong, James
 , TITLE OF INVENTION: Defensin Polynucleotides and Methods of
 , TITLE OF INVENTION: Use
 , FILE REFERENCE: 35718/2467C3
 , CURRENT APPLICATION NUMBER: US/10/178,213
 , CURRENT FILING DATE: 2002-06-21
 , PRIOR APPLICATION NUMBER: 60/300,152
 , PRIOR FILING DATE: 2001-06-22
 , PRIOR APPLICATION NUMBER: 60/100,241
 , PRIOR FILING DATE: 2001-06-22
 , NUMBER OF SEQ ID NOS: 469
 , SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 411
 LENGTH: 47
 TYPE: PRT
 ORGANISM: *Tropaeculum majus*
 US-10-178-213-411

Alignment Scores:
 Pred. No.: 1.84 Length: 47
 Score: 71.66 Matches: 14
 Percent Similarity: 50.00% Conservative: 5
 Best Local Similarity: 36.84% Mismatches: 13
 Query Match: 21.91% Indels: 6
 DB: 15 Gaps: 2

US-09-673-274B-2 (1-169) × US-10-178-213-411 (1-47)

Qy 13 GGTCTCGTGGTGTGAACTACACTCCGATTGCAACGGTGACTGCCAGAGGAGG 72
 Db 12 GlyProCysAlaSerValCysLyStar 26

Qy 73 PGGGTTCAGGGTGGTCACTGGTTCCCTAACGTGAATCTGCTGGTGC :26
 Db 27 GluGlyPheTyrGlyLysCysArgGlyPheArgHis--ArgCysPheCys 43

RESULT 14
 US-10-178-213-410
 , Sequence 410, Application US/10178213
 , Publication No. US2003041348A1
 , GENERAL INFORMATION:
 , APPLICANT: Simmons, Carl R.
 , APPLICANT: Navarro Acevedo, Pedro A.
 , APPLICANT: Harvell, Leslie
 , APPLICANT: Cahoon, Rebecca
 , APPLICANT: McCuchen, Billy Fred
 , APPLICANT: Lu, Albert
 , APPLICANT: Herrmann, Rafael
 , APPLICANT: Wong, James
 , TITLE OF INVENTION: Defensin Polynucleotides and Methods of
 , TITLE OF INVENTION: Use
 , FILE REFERENCE: 35718/2467C3
 , CURRENT APPLICATION NUMBER: US/10/178,213
 , CURRENT FILING DATE: 2002-06-21
 , PRIOR APPLICATION NUMBER: 60/300,152
 , PRIOR FILING DATE: 2001-06-22
 , PRIOR APPLICATION NUMBER: 60/300,241
 , PRIOR FILING DATE: 2001-06-22
 , NUMBER OF SEQ ID NOS: 469
 , SOFTWARE: FastSEQ for Windows Version 4.0

GenCore version 5.1.6
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DM nucleic - protein search, using frame_Plus_n2p model

Run on: October 16, 2003, 17:06:37 ; Search time 16.8439 Seconds
(without alignments)
849.038 MillNon celi. updates/sec

Title: US-09-673-274B-2

Perfect score: 324

Sequence: 1 gataaaggatcgatccctg.....gaacgtgtcgacggatccgg 169

Scoring table: BL21562

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 657434

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-O:/cgn2_1/uspro/spool/US09673214/runat16:02063.170628.2580/app/query.fasta_1.654

-DE/Issued_Patents_AA -QMT=fastcan -SUFFIX=rai -MINMATCH=0.1 -LOEFL=0

-LIST=45 -LOCAL_OUTMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000

-MOL=MAP -DOCALIGN=200 -THR SCORE=PCT -END=1 -MATRX=blosum62 -TRANS=human40.cdi

-NO_MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG

-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRAD=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6

-FGAPEXT=7 -YGAPOP=10 -YGAPPXT=0.5 -DELOP=6 -DELEXT=7

Issued_Patents_AA:*

1: /cgn2_6/podata/1/iaa/SA_COMBO.pep:*

2: /cgn2_6/podata/1/iaa/5B_COMBO.pep:*

3: /cgn2_6/podata/1/iaa/6A_COMBO.pep:*

4: /cgn2_6/podata/1/iaa/6B_COMBO.pep:*

5: /cgn2_6/podata/1/iaa/PCFUS_COMBO.pep:*

6: /cgn2_6/podata/1/iaa/backfile1.pep:*

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the total, score distribution, and is derived by analysis of the tota: score distribution.

SUMMARIES

| Result No. | Score | Query | Match Length | DB ID | Description |
|------------|-------|-------|--------------|---------------------------|--------------------------------|
| c 1 | 81.5 | 26.9 | 280 | 4 US-09-252-991A-19400 | Sequence 19400; Sequence 19400 |
| c 2 | 80.5 | 24.8 | 65 | 1 US-08-435-040-2 | Sequence 2, App1 |
| c 3 | 80.5 | 24.8 | 65 | 3 US-02-216-1 | Sequence 2, App1 |
| c 4 | 78 | 25.7 | 149 | 4 US-09-252-991A-32270 | Sequence 32270, A |
| c 5 | 76.5 | 23.6 | 61 | 1 US-08-682-85A-25 | Sequence 25, App1 |
| c 6 | 76.5 | 23.6 | 61 | 1 US-08-451-472-4 | Sequence 4, App1 |
| c 7 | 76.5 | 23.6 | 61 | 2 US-08-931-314-25 | Sequence 25, App1 |
| c 8 | 75 | 23.1 | 64 | 4 US-08-403-343B-25 | Sequence 25, App1 |
| c 9 | 74.5 | 23.0 | 44 | 4 US-08-251-4 | Sequence 4, App1 |
| c 10 | 74.5 | 23.0 | 69 | 4 US-09-480-251-6 | Sequence 6, App1 |
| c 11 | 74.5 | 23.0 | 70 | 4 US-09-480-251-2 | Sequence 2, App1 |
| c 12 | 73.5 | 24.3 | 158 | 4 US-09-252-991A-26807, A | Sequence 26807, A |

US-09-252-991A-19400

Sequence 22334, A
Sequence 17266, A
Sequence 26857, A
Sequence 16810, A
Sequence 32162, A
Sequence 6, App1
Sequence 3, App1
Sequence 3, App1
Sequence 2303, A
Sequence 20063, A
Sequence 31970, A
Sequence 27028, A
Sequence 20293, A
Sequence 26207, A
Sequence 26207, A
Sequence 28844, A
Sequence 18128, A
Sequence 19367, A
Sequence 14, App1
Sequence 273, A
Sequence 2273, A
Sequence 1914, A
Sequence 26, App1
Sequence 16536, A
Sequence 18432, A
Sequence 19528, A
Sequence 17589, A
Sequence 31377, A
Sequence 32675, A
Sequence 26994, A
Sequence 20796, A
Sequence 23611, A

ALIGNMENTS

RESULT 1
US-09-252-991A-19400
Sequence 19400, Application US-09-252-991A-19400
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenstein et al.
TITLE OF INVENTION: PERUGNCNA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 10716-136
CURRENT APPLICATION NUMBER: US-09-252-991A-19400
CURRENT FILING DATE: 1999-01-18
PRIOR APPLICATION NUMBER: US-09-252-991A-19400
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NCS: 33142
SEQ ID NO 19400
LENGTH: 280
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19400

QY 100 AACCGAGTGAACCCATTGT-----ACCTCCTCTTG-----AC: 62
 DB 200 ArgGala-----AiaGlyArgGlyLysProGlySerGlyCysArgTrpCys 217
 Sequence 2, Application US/08435040
 Patent No. 5756340

GENERAL INFORMATION:
 APPLICANT: Hammock, Bruce J.
 ADDRESS: Moskowitz, Haim
 STREET: Four Embarcadero Center, Suite 1150
 CITY: San Francisco
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 94111-4121

TITLE OF INVENTION: Insect Control With Multiple Toxins
 NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Majestic, Parsons, Siebert & Hsue
 STREET: Four Embarcadero Center, Suite 1150
 CITY: San Francisco
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 94111-4121

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DCS/MS-DCS
 SOFTWARE: Patent In Release #1.0, Version #1.25

APPLICATION NUMBER: US/08/435.340
 FILING DATE: 08-MAY-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Siebert, J. Suzanne
 REFERENCE/DOCKET NUMBER: 28-758
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 362-5556
 TELEX: 278638 MGPS
 INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
 LENGTH: 65 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 US-09-020-216-2

ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 US-09-020-216-2

Alignment Scores:
 Pred. No.: 0.0254
 Score: 80.50
 Percent Similarity: 57.14%
 Best Local Similarity: 40.48%
 Query Match: 24.85%
 DB: 12 AsnCysValTyrThrCysGlyAlaAsnSerTyr-----

Length: 65
 Matches: 17
 Conservative: 7
 Missmatches: 9
 Indels: 9
 Gaps: 4

US-09-673-274B-2 (1-16): x US-09-020-216-2 (1-65)

QY 16 TCCCTGGCTGG-----GGTGGCTGGAACTACACTTUGATTGCAACGGTAGTCAG 69
 DB 12 AsnCysValTyrThrCysGlyAlaAsnSerTyr-----
 QY 70 AGGAGGGTTAACGGTGGTCACTGC-----GTTCTCTTCGTAAGTGAAGTGC 120
 DB 29 LysAsnGlyAlaGluSerGlyTyroCysGlnTrpPheGlyLysTrpPheGlyLysTrp 47
 QY 121 TGGTC 126
 DB 48 TrpCys 49

RESULT 3
 US-09-020-216-2
 Sequence 2, Application US/09020216
 Patent No. 6-643C
 GENERAL INFORMATION:
 APPLICANT: Hammock, Bruce J.
 ADDRESS: Herrmann, Rafael D.
 APPLICANT: Moskowitz, Haim
 TITLE OF INVENTION: Insect Control With Multiple Toxins
 NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Majestic, Parsons, Siebert & Hsue
 STREET: Four Embarcadero Center, Suite 1150
 CITY: San Francisco
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 94111-4121

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DCS
 SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/020,216
 FILING DATE:

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/435.340
 FILING DATE: 08-MAY-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Siebert, J. Suzanne
 REFERENCE/DOCKET NUMBER: 28-758
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 362-5556
 TELEX: 278638 MGPS
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 65 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 US-09-020-216-2

Alignment Scores:
 Pred. No.: 0.0254
 Score: 80.50
 Percent Similarity: 57.14%
 Best Local Similarity: 40.48%
 Query Match: 24.85%
 DB: 12 AsnCysValTyrThrCysGlyAlaAsnSerTyr-----
 Length: 65
 Matches: 17
 Conservative: 7
 Missmatches: 9
 Indels: 9
 Gaps: 4

US-09-673-274B-2 (1-16): x US-09-020-216-2 (1-65)

QY 16 TCCCTGGCTGG-----GGTGGCTGGAACTACACTTUGATTGCAACGGTAGTCAG 69
 DB 12 AsnCysValTyrThrCysGlyAlaAsnSerTyr-----
 QY 70 AGGAGGGTTAACGGTGGTCACTGC-----GTTCTCTTCGTAAGTGAAGTGC 120
 DB 29 LysAsnGlyAlaGluSerGlyTyroCysGlnTrpPheGlyLysTrpPheGlyLysTrp 47
 QY 121 TGGTC 126
 DB 48 TrpCys 49

RESULT 4

IS-09-252-991A-32270 Sequence 32270, Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: 107196.136
 CURRENT APPLICATION NUMBER: US/09/252.991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 SEQ ID NO: 32270
 LENGTH: 149
 TYPE: PRT
 ORGANISM: *Pseudomonas aeruginosa*
 IS-09-252-991A-32270

Alignment Scores:

| Ref. No.: | Length: | Score: | Matches: | Conservative: | Mismatch: | Indels: | Gaps: |
|--|---------|--------|----------|---------------|-----------|---------|-------|
| core: | 0.0607 | 149 | 78 | 18 | 8 | 21 | 2 |
| est: | 49.061 | | | | | | |
| est Local Similarity: | 33.964 | | | | | | |
| Query Match: | 25.744 | | | | | | |
| DB: | 4 | | | | | | |
| 14 ProSerProAlaSerArgArgArgCysSerProArgSerProThrGly--- | 32 | | | | | | |
| 109 TAGCGAACGAACCGCACTGACCACCCCTGTAAACCCCTCTTGACTCACCGTCAAT 50 | | | | | | | |
| 33 --ArgTyrThrArgAlaProTrpArgCys-----cysArgArgArgCysArg 47 | | | | | | | |
| Db: | | | | | | | |
| 109 TAGCGAACGAACCGCACTGACCACCCCTGTAAACCCCTCTTGACTCACCGTCAAT 50 | | | | | | | |
| 33 --ArgTyrThrArgAlaProTrpArgCys-----cysArgArgArgCysArg 47 | | | | | | | |
| Db: | | | | | | | |
| 49 CGGAAGTGTAGTTCACAGCACCCCCACAGCGAACCGA 11 | | | | | | | |
| 48 ArgArgCysArgProArgProArgProThrSerLysAlaArg 60 | | | | | | | |
| Db: | | | | | | | |

RESULT 5
 IS-08-482-485A-25
 Sequence 25, Application US/08682485A
 Patent No. 5763568
 GENERAL INFORMATION:
 APPLICANT: ATKINSON, RONALD K.
 APPLICANT: HOWDEN, MERLIN E. H.
 APPLICANT: VONARX, EDWARD J.
 TITLE OF INVENTION: Insecticidal Toxins Derived From Spiders
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Zeneca, Inc.
 STREET: 1200 South 47th Street
 CITY: Richmond
 STATE: California
 COUNTRY: USA
 ZIP: 94804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/682,485
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/682,485

106 CCTAACCTGAACTGCTGGAGACTTGAGAGTCGGCGAAGGCCAACGTTGTCGAGGT 165
 :::::|||:|||:|||:|||:|||:|||:
 40 SerGlyIleAlaCysTrpCysAsn-----AspLeuProGluAsnValProIleysAsp 57

b 166 CCG 168
 |||
 58 Pro 58

RESULT 9
 Sequence 4 , Application US/0948025;

GENERAL INFORMATION:
 Patent No. 6455719

APPLICANT: DeRose, Richard

APPLICANT: Freyssinet, Georges

PRIOR APPLICATION NUMBER: PCT/FR98/01462

CURRENT FILING DATE: 2000-01-11

PRIOR APPLICATION NUMBER: PCT/FR98/01462

PRIOR FILING DATE: 1998-07-08

PRIOR APPLICATION NUMBER: FRANCE 97/09,115

PRIOR FILING DATE: 1997-07-11

PRIOR APPLICATION NUMBER: FRANCE 9709,663

PRIOR FILING DATE: 1997-07-24

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 4

LENGTH: 44

TYPE: PRT

ORGANISM: Drosophila melanogaster

JS-09-480-251-4

Alignment Scores:
 Pred. No.: 0.138
 Score: 74.50

Percent Similarity: 42.50%

Best Local Similarity: 37.50%

Query Match: 22.9%

DB: 1B:

Length: 44

Matches: 15

Conservative: 16

Mismatches: 7

Indels: 3

Gaps: 3

RESULT 10
 Sequence 6 , Application US/09480251

Patent No. 6465719

GENERAL INFORMATION:

APPLICANT: DeRose, Richard

APPLICANT: Freyssinet, Georges

PRIOR APPLICATION NUMBER: PCT/FR98/01462

CURRENT FILING DATE: 2000-01-11

PRIOR APPLICATION NUMBER: PCT/FR98/01462

PRIOR FILING DATE: 1998-07-08

PRIOR APPLICATION NUMBER: FRANCE 97/09,115

PRIOR FILING DATE: 1997-07-11

PRIOR APPLICATION NUMBER: FRANCE 9709,663

PRIOR FILING DATE: 1997-07-24

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 2

LENGTH: 70

TYPE: PRT

ORGANISM: Drosophila melanogaster

US-09-480-251-6

Alignment Scores:
 Pred. No.: 0.149
 Score: 74.50

Percent Similarity: 42.50%

Best Local Similarity: 37.50%

Query Match: 22.9%

DB: 4

Length: 70

Matches: 15

Conservative: 2

Mismatches: 16

Indels: 7

Gaps: 3

RESULT 11
 Sequence 11 , Application US/09-480-251-6

Patent No. 6465719

GENERAL INFORMATION:

APPLICANT: DeRose, Richard

APPLICANT: Freyssinet, Georges

PRIOR APPLICATION NUMBER: PCT/FR98/01462

CURRENT FILING DATE: 2000-01-11

PRIOR APPLICATION NUMBER: PCT/FR98/01462

PRIOR FILING DATE: 1998-07-08

PRIOR APPLICATION NUMBER: FRANCE 97/09,115

PRIOR FILING DATE: 1997-07-11

PRIOR APPLICATION NUMBER: FRANCE 9709,663

PRIOR FILING DATE: 1997-07-24

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 11

LENGTH: 69

TYPE: PRT

ORGANISM: The ubiquitin - diosomycin fusion peptide

US-09-480-251-6

Alignment Scores:
 Pred. No.: 0.149
 Score: 74.50

Percent Similarity: 42.50%

Best Local Similarity: 37.50%

Query Match: 22.9%

DB: 3

Length: 69

Matches: 15

Conservative: 2

Mismatches: 16

Indels: 7

Gaps: 3

RESULT 12
 Sequence 12 , Application US/09-480-251-6

Patent No. 6465719

GENERAL INFORMATION:

APPLICANT: DeRose, Richard

APPLICANT: Freyssinet, Georges

PRIOR APPLICATION NUMBER: PCT/FR98/01462

CURRENT FILING DATE: 2000-01-11

PRIOR APPLICATION NUMBER: PCT/FR98/01462

PRIOR FILING DATE: 1998-07-08

PRIOR APPLICATION NUMBER: FRANCE 97/09,115

PRIOR FILING DATE: 1997-07-11

PRIOR APPLICATION NUMBER: FRANCE 9709,663

PRIOR FILING DATE: 1997-07-24

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 12

LENGTH: 70

TYPE: PRT

ORGANISM: Glycine max

US-09-480-251-6

Alignment Scores:
 Pred. No.: 0.149
 Score: 74.50

Percent Similarity: 42.50%

Best Local Similarity: 37.50%

Query Match: 22.9%

DB: 4

Length: 70

Matches: 15

Conservative: 2

Mismatches: 16

Indels: 7

Gaps: 3

RESULT 13
 Sequence 13 , Application US/09-480-251-6

Patent No. 6465719

GENERAL INFORMATION:

APPLICANT: DeRose, Richard

APPLICANT: Freyssinet, Georges

PRIOR APPLICATION NUMBER: PCT/FR98/01462

CURRENT FILING DATE: 2000-01-11

PRIOR APPLICATION NUMBER: PCT/FR98/01462

PRIOR FILING DATE: 1998-07-08

PRIOR APPLICATION NUMBER: FRANCE 97/09,115

PRIOR FILING DATE: 1997-07-11

PRIOR APPLICATION NUMBER: FRANCE 9709,663

PRIOR FILING DATE: 1997-07-24

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 13

LENGTH: 70

TYPE: PRT

ORGANISM: Glycine max

US-09-480-251-6

Alignment Scores:
 Pred. No.: 0.149
 Score: 74.50

Percent Similarity: 42.50%

Best Local Similarity: 37.50%

Query Match: 22.9%

DB: 4

Length: 70

Matches: 15

Conservative: 2

Mismatches: 16

Indels: 7

Gaps: 3

RESULT 14
 Sequence 14 , Application US/09-480-251-6

Patent No. 6465719

GENERAL INFORMATION:

APPLICANT: DeRose, Richard

APPLICANT: Freyssinet, Georges

PRIOR APPLICATION NUMBER: PCT/FR98/01462

CURRENT FILING DATE: 2000-01-11

PRIOR APPLICATION NUMBER: PCT/FR98/01462

PRIOR FILING DATE: 1998-07-08

PRIOR APPLICATION NUMBER: FRANCE 97/09,115

PRIOR FILING DATE: 1997-07-11

PRIOR APPLICATION NUMBER: FRANCE 9709,663

PRIOR FILING DATE: 1997-07-24

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 14

LENGTH: 70

TYPE: PRT

ORGANISM: Glycine max

US-09-480-251-6

Alignment Scores:
 Pred. No.: 0.149
 Score: 74.50

Percent Similarity: 42.50%

Best Local Similarity: 37.50%

Query Match: 22.9%

DB: 4

Length: 70

Matches: 15

Conservative: 2

Mismatches: 16

Indels: 7

Gaps: 3

RESULT 15
 Sequence 15 , Application US/09-480-251-6

Patent No. 6465719

GENERAL INFORMATION:

APPLICANT: DeRose, Richard

APPLICANT: Freyssinet, Georges

PRIOR APPLICATION NUMBER: PCT/FR98/01462

CURRENT FILING DATE: 2000-01-11

PRIOR APPLICATION NUMBER: PCT/FR98/01462

PRIOR FILING DATE: 1998-07-08

PRIOR APPLICATION NUMBER: FRANCE 97/09,115
 PRIOR FILING DATE: 1997-07-11

PRIOR APPLICATION NUMBER: FRANCE 9709,663

PRIOR FILING DATE: 1997-07-24

NUMBER OF SEQ ID NOS: 15

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO: 15

LENGTH: 70

TYPE: PRT

ORGANISM: Glycine max

US-09-480-251-6

Alignment Scores:
 Pred. No.: 0.149
 Score: 74.50

Percent Similarity: 42.50%

Best Local Similarity: 37.50%

Query Match: 22.9%

DB: 4

Length: 70

Matches: 15

Conservative: 2

Mismatches: 16

Indels: 7

Gaps: 3

RESULT 12
 Jb 51 GlyGlyArgSerSerGlyHisSer----ProSerLysCysTrpCysGlu 68
 Sequence 22334 Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 FILE REFERENCE: 107196-136
 CURRENT APPLICATION NUMBER: US/09/252,991-A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 63/C74,788
 PRIOR FILING DATE: 1998-01-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO: 26807
 LENGTH: 158
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-268C7

Alignment Scores:
 Pred. No.: C-23 Length: 158
 Score: 73.50 Matches: 21
 Percent Similarity: 47.46% Conservative: 7
 Best Local Similarity: 35.59% Mismatches: 16
 Query Match: 24.26% Indexes: 15
 DB: 4 Gaps: 4

Jb 169 CGGGATCCGTGCGACAGTCGGCTCGCGTGAAGTCGACCAAGCTTCAGT 110
 Qy 42 ... -----LysThrSerProCysGlyThrGlySerAlaAlaThrArgCys 57
 Jb 26 ProSerProAlaThrArgLysProArg-----SerProSerAlaSerAlaS 41

Qy 109 TAGCGAGGAACCGCAACTGGCACTTGTAACCCC-----ProCTCTGCACCTGGACTTACCGCTGC 53
 Jb 52 AACGG-----ANGCTGAGTTCAAGCACCACACGGGAC 14
 Jb 58 GlyArgProSerAlaLysArgSerProCysProSerAlaSerProSerArgAsn 76

RESULT 13
 US-09-673-274B-2 (1-169) x US-09-252-991A-268C7 (1-158)
 Sequence 22334 Application US/09252991A
 Patent No. 6551795
 GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 FILE REFERENCE: 107196-136
 CURRENT APPLICATION NUMBER: US/09/252,991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 63/C74,788
 PRIOR FILING DATE: 1998-01-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO: 22334
 LENGTH: 145
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa

Alignment Scores:
 Pred. No.: 0.262 Length: 145
 Score: 73.00 Matches: 22
 Percent Similarity: 45.76% Conservative: 5

Best Local Similarity: 37.29% Missmatches: 22
 Query Match: 24.09% Indexes: 10
 DB: 4 Gaps: 3

US-09-673-274B-2 (1-169) x JS-09-252-991A-22334 (1-145)

Qy 163 CGCTCGAACACGCTCGCTCGCCGAGCTCTCAAGTCT----CGCACAGGAGTCACCT 110
 Jb 52 ProSerAlaArgLysAlaArgProArgLeuArgSerProProArgSerGlnAlaGlyLys 71
 Qy 109 TAGCGAGGAACCGCACTGGACTTACGCCCTGTAACCCC-----TCTTCG 65
 Jb 72 ValArgArgAlaProArgArgProCysAsnProSerArgAlaProSerThrSerCys 91
 Qy 64 ACTACCGT-----TGCAATCGAAAGTAGTCACGACCCCCACAGCAG 17
 Jb 92 AlaCysArgSerProAlaArgSerProThrProProProArg 110

RESULT 14
 US-09-252-991A-17266
 Sequence 17266 Application US/09252991A
 Patent No. 6551795

GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 FILE REFERENCE: 107196-136
 CURRENT APPLICATION NUMBER: US/09/252-991A
 CURRENT FILING DATE: 1999-02-18
 PRIOR APPLICATION NUMBER: US 60/074,788
 PRIOR FILING DATE: 1998-02-18
 PRIOR APPLICATION NUMBER: US 60/094,190
 PRIOR FILING DATE: 1998-07-27
 NUMBER OF SEQ ID NOS: 33142
 SEQ ID NO: 17266
 LENGTH: 248
 TYPE: PRT
 ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-17266

Alignment Scores:
 Pred. No.: 0.445 Length: 248
 Score: 71.50 Matches: 18
 Percent Similarity: 44.44% Conservative: 6
 Best Local Similarity: 33.33% Mismatches: 17
 Query Match: 23.60% Indexes: 13
 DB: 4 Gaps: 2

US-09-673-274B-2 (1-169) x US-09-252-991A-17266 (1-248)

Qy 163 CGCTCGAACACGCTCGCTCGCCGAGCTCTCAAGTCT----GCTCTCAAAGTCTCCACCCAGCTTC 113
 Jb 39 ProAlaArgAlaGlyArgAlaAlaThrLeuArgInArgAspProGluSer 58
 Qy 212 CGTAGCGAGGAACGGAGTGTGACCCCTCTGTAACCCCTCCCTGACTACCGTGC 53
 Jb 59 ArgAlaAspArgArg-----LeuArgArgCys 68

RESULT 15
 US-09-252-991A-268C7
 Sequence 26857 Application US/09252991A
 Patent No. 6551795

GENERAL INFORMATION:
 APPLICANT: Marc J. Rubenfield et al.
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 FILE REFERENCE: 107196-136
 CURRENT APPLICATION NUMBER: US/09/252-991A
 CURRENT FILING DATE: 1999-02-18

Qy 52 AATGGAGCTGAGTCAGCACCACACGGGAC 11
 Jb 69 ArgAlaArgGlyArgLysProAlaArgProGlyArg 82

PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
SEQ ID NO: 28857
SQ ID NOS: 13142

LENGTH: 397
TYPE: PRT
ORGANISM: *Pseudomonas aeruginosa*
ID: 352-0015-26857

Search completed: October 16, 2003, 17:13:05
Search time: 18.8439 secs

GenCore version 5.1.6
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DM nucleic - protein search, using frame_plus_n2p model

Run on: October 16, 2003, 17:06:37 : Search time 16.2259 Seconds

(without alignments)
1564.690 Million cell updates/sec

Title: US-09-673-274B-2_COPY_1_132

Perfect score: 1777

Sequence: 1 gataaagtatcggttccctg.....rgaaatgtctggcgagact 132

Scoring table: BL00DM62

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|--------|------|---------|-----|
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| Ygapop | 10.0 | Ygapext | 0.5 |
| Fgapop | 6.0 | Fgapext | 7.0 |
| Delop | 6.0 | Delext | 7.0 |

Searched: 283308 seqs, 9616868 residues

Total number of hits satisfying chosen parameters: 566616

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-iQ=/cgn2/1/uspto/spool/US09673274/runat_16102003_170628_2555/app/query.fasta_1.654
-iDB=PIR_76 -QFMT=fastan -SUFFIX=PIR -MINMATCH=0.7 -LOOPEXT=0
-nUNITS=6its -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40_cdi -LIST=45
-nDOCALIGN=200 -nTUR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=40 -CDI -LIST=45
-nOUTFORMAT=PIR -NORM=EXT -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-nOUTFORMAT=PIR -NORM=EXT -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-nNO_MMAPP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-nDEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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Database: PIR_76::

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1: pir1::  
2: pir2::  
3: pir3::  
4: pir4::
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Match | Length | DB ID | Description |
|------------|-------|-------|-------|--------|--------|---------------------|
| 1 | 86 | 32.2 | 66 | 2 | A29386 | neurotoxin III - 6 |
| 2 | 80.5 | 30.1 | 65 | 2 | A59222 | neurotoxin X - sco |
| 3 | 79.5 | 29.8 | 66 | 2 | A55859 | crustacean-specific |
| 4 | 79 | 29.6 | 85 | 2 | S6896 | alpha-toxin Bot XI |
| 5 | 78.5 | 29.4 | 84 | 1 | NTSR1A | neurotoxin III Pre |
| 6 | 77.5 | 29.0 | 65 | 1 | NTSR1I | neurotoxin IV - Eg |
| 7 | 76.5 | 28.7 | 61 | 2 | B34133 | depressant insect |
| 8 | 76 | 28.5 | 66 | 1 | NTSR1E | neurotoxin M14 - 1 |
| 9 | 75.5 | 28.3 | 65 | 1 | NTSR1C | neurotoxin 1 - bar |
| 10 | 74.5 | 27.9 | 70 | 2 | A55814 | drosomycin precurs |
| 11 | 74 | 27.7 | 59 | 2 | C2377 | neurotoxin V-5 - b |
| 12 | 74 | 27.7 | 64 | 2 | JC1321 | neurotoxin IV - Sa |
| 13 | 73 | 27.3 | 64 | 1 | NTSR1L | neurotoxin V - Egy |
| 14 | 70.5 | 26.4 | 65 | 1 | NTSR2K | neurotoxin 3 - bar |

RESULT 2

```
A59222
neurotoxin X - scorpion (Leiurus quinquestratus)
C;Species: Leiurus quinquestratus hebraeus
```

| Score | Length | DB | ID | Description |
|-------|--------|----|--------|-----------------------|
| 87 | 26.4 | 1 | JNC670 | Na+-channel-blocker |
| 84 | 26.0 | 1 | NTSR2N | Na+-channel-blocker |
| 62 | 25.7 | 2 | D59352 | depressant insect- |
| 66 | 25.7 | 1 | NTSR9E | neurotoxin I - le |
| 83 | 25.7 | 1 | NTSR5M | neurotoxin V |
| 64 | 25.5 | 1 | NTSR5M | protease inhibitor |
| 77 | 25.3 | 2 | T4395 | depressant insect- |
| 61 | 25.3 | 2 | B59352 | depressant insect- |
| 61 | 25.3 | 2 | C59352 | depressant insect- |
| 83 | 25.3 | 1 | JN0669 | Na+-channel-blocker |
| 86 | 25.1 | 2 | JN0671 | Na+-channel-blocker |
| 66 | 24.9 | 1 | NTSR1B | neurotoxin 2 - bar |
| 66 | 24.7 | 2 | T2433 | hypothetical protein |
| 61 | 24.5 | 2 | T374 | probable laminin a |
| 66 | 24.2 | 2 | A59026 | excitatory insect- |
| 66 | 24.2 | 2 | B2727 | neurotoxin V-4 |
| 85 | 23.8 | 2 | A40472 | depressant insect |
| 64 | 24.0 | 2 | S10578 | protease inhibitor |
| 78 | 24.0 | 2 | S52634 | gamma-thionin |
| 92 | 24.0 | 2 | S43228 | defensin - fruit |
| 85 | 23.8 | 2 | A40472 | depressant insect |
| 64 | 23.6 | 2 | A35940 | neurotoxin Iipb-1 |
| 85 | 23.6 | 2 | A39306 | alpha insect toxin |
| 78 | 23.2 | 2 | S18253 | LDL receptor related |
| 65 | 23.0 | 1 | NTSR2B | laminin alpha-1 chain |
| 65 | 23.0 | 2 | A38394 | neurotoxin AAH IT4 |
| 66 | 23.0 | 2 | A27406 | toxin CSS-1 - Mex |
| 84 | 23.0 | 2 | JE0143 | anti-mammals neuro |

ALIGNMENTS

RESULT 1

A29386

neurotoxin III - SCORPION (Buttus occitanus)

C;Species: Buttus occitanus madochaei

C;Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 07-Feb-1997

C;Accession: A29386

R;Vargas, O.; Martin, M.F.; Rochat, H.

Eur. J. Biochem. 162, 589-599, 1987

A;Title: Characterization of six toxins from the venom of the Moroccan scorpion Buttus

A;Reference number: A29386; PMID:3104356

A;Accession: A29386

A;Molecule type: Protein

A;Residues: 1-662

C;Superfamily: scorpion: neurotoxin

C;Keywords: neurotoxin

Alignment Scores:

Pred. No.: 0.0247

Score: 86.00

Percent Similarity: 55.00%

Best Local Similarity: 37.50%

Query Match: 32.21%

DB: 2

Length: 66

Matches: 15

Conservative: 7

Mistmatches: 16

Indels: 2

Gaps: 1

US-09 673-274B-2_COPY_1_132 (1-132) x A29386 (1-66)

C;Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 19-Apr-2002

C;Accession: A59222 alpha-toxin, P.; Nakajima, T. Butus occitanus

R;Corzo, G.; Escudero, P.; Nakajima, T. alpha-toxin precursor - scorpion (Butus occitanus)

Submitted to the Protein Sequence Database, April 2000

A;Description: A procedure for the rapid purification of non commercial and new scorpion

A;Reference number: A59222 C;Species: Butus occitanus tunetanus

A;Accession: A59222 C;Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 16-Jul-1999

R;Bouhala-Zahar, B.; Ducarne, F.; ben Khalifa, I.; ben Borhani, L.; Pe: C;Accession: S68906 R;Bouhala-Zahar, B.; Ducarne, F.; ben Khalifa, I.; ben Borhani, L.; Pe: Eur. J. Biochem. 238, 653-660, 1996

A;Title: A recombinant insect-specific alpha-toxin of *Butus occitanus tunetanus* score

A;Reference number: S68906 MCID:9630228; PMID:870664

A;Accession: S68906 A;Status: Preliminary

A;Molecule type: protein A;Cross-references: GB:X32376; NID:91041277; PID:CAA63120.1; PID:gi041278

C;Superfamily: scorpion neurotoxin A;Residues: i-65 <COR>

C;Keywords: amide carboxyl end; neurotoxin; venom A;Status: predicted

F:13-64,-7-37,23-47,27-49/Disulfide bonds: #status predicted

F:65/Modified site: amidated carboxy; end (Arg); #status predicted

Alignment Scores:

Pred. No.: 0.117

Score: 65

Percent Similarity: 50.50

Best Local Similarity: 57.14%

Query Match: 30.15%

DB: 2

Length: 65

Matches: 57

Conservative: 7

Mismatches: 9

Indels: 9

Gaps: 4

C;Sequence: US-09 673-274B-2_COPY_1_132 (1-132) x A59222 (1-65)

C;Sequence: 16 TCCCTGGTGTGG-----GTTGCTGTGAATACACTTCCGATGCAAGGTGAGTGCAG 69

C;Sequence: 22 AsnCysValtryrThrCysGlyAlaLysSerIle...-cysAsnThrGlyCys-His: 28

C;Sequence: 70 AGGAGGGTACAAGGGTGTACTGC-----GGTTCTCTGCTAACGTAACCTGC 120

C;Sequence: 29 LysAsnGlyAlaGluSerGlyTyrCysGlnrpoteGlyLysTrpGlyAsnAla---cys 47

C;Sequence: 121 TGGTGC 126

C;Sequence: 46 TripCys 49

C;Sequence: 19 TGGTGTGGTGTCTGCAACTACACTTCCGATGCAAGGTGAGTCAG 7B

C;Sequence: 16 CyPherPheLeuglylAsn-----GluasnCysAspIysGluCysLysAlaLysAsn 33

C;Sequence: 79 TAAGGCT-----GGTCATCGGGTCCGTACCTGCTAACCTGCTGGCCAG 129

C;Sequence: 34 GlnGlyGlySerGlyTyrCysTyrSerIleAla-----CystePheAla 49

C;Sequence: 19 TGGTGTGGTGTCTGCAACTACACTTCCGATGCAAGGTGAGTCAG 7B

C;Sequence: 16 CyPherPheLeuglylAsn-----GluasnCysAspIysGluCysLysAlaLysAsn 33

C;Sequence: 79 TAAGGCT-----GGTCATCGGGTCCGTACCTGCTAACCTGCTGGCCAG 129

C;Sequence: 34 GlnGlyGlySerGlyTyrCysTyrSerIleAla-----CystePheAla 49

RESULT 4

S68906

alpha-toxin Bot XIV precursor - scorpion (Butus occitanus)

C;Species: Butus occitanus tunetanus

C;Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 16-Jul-1999

R;Bouhala-Zahar, B.; Ducarne, F.; ben Khalifa, I.; ben Borhani, L.; Pe: C;Accession: S68906

R;Corzo, G.; Escudero, P.; Nakajima, T. alpha-toxin precursor - scorpion (Butus occitanus)

A;Accession: S68906 A;Status: Preliminary

A;Molecule type: mRNA A;Cross-references: GB:X32376; NID:91041277; PID:CAA63120.1; PID:gi041278

A;Residues: i-65 <COR>

A;Keywords: amide carboxyl end; neurotoxin; venom

A;Status: predicted

F:13-64,-7-37,23-47,27-49/Disulfide bonds: #status predicted

F:65/Modified site: amidated carboxy; end (Arg); #status predicted

Alignment Scores:

Pred. No.: 0.117

Score: 65

Percent Similarity: 50.48%

Best Local Similarity: 57.14%

Query Match: 30.15%

DB: 2

Length: 65

Matches: 57

Conservative: 7

Mismatches: 9

Indels: 9

Gaps: 4

C;Sequence: US-09 673-274B-2_COPY_1_132 (1-132) x S68906 (1-95)

C;Sequence: 16 TCCTGCGTGGGGTGTGGTGTACTCCGATTGCCAACGGTCAAGGGAGGG 75

C;Sequence: 29 AspCysAlaGlySerGlyTyrCysGlnrpoteGlyLysTrpGlyAsnIle 48

C;Sequence: 76 GGTACAGGGGGGTCACTGGGT----TCCCTGGCTAACGTAACGTGAACTGTGGTGCAG 129

C;Sequence: 49 GlyA:amrSerGlyHisCysGlyHisLysSerGlySerGlyHisGly 49

C;Sequence: 19 TGGTGTGGTGTCTGCAACTACACTTCCGATGCAAGGTGAGTCAG 7B

C;Sequence: 16 CyPherPheLeuglylAsn-----GluasnCysAspIysGluCysLysAlaLysAsn 33

C;Sequence: 79 TAAGGCT-----GGTCATCGGGTCCGTACCTGCTAACCTGCTGGCCAG 129

C;Sequence: 34 GlnGlyGlySerGlyTyrCysTyrSerIleAla-----CystePheAla 49

C;Sequence: 19 TGGTGTGGTGTCTGCAACTACACTTCCGATGCAAGGTGAGTCAG 7B

C;Sequence: 16 CyPherPheLeuglylAsn-----GluasnCysAspIysGluCysLysAlaLysAsn 33

C;Sequence: 79 TAAGGCT-----GGTCATCGGGTCCGTACCTGCTAACCTGCTGGCCAG 129

C;Sequence: 34 GlnGlyGlySerGlyTyrCysTyrSerIleAla-----CystePheAla 49

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C;Sequence: 16 CyPherPheLeuglylAsn-----GluasnCysAspIysGluCysLysAlaLysAsn 33

C;Sequence: 79 TAAGGCT-----GGTCATCGGGTCCGTACCTGCTAACCTGCTGGCCAG 129

C;Sequence: 34 GlnGlyGlySerGlyTyrCysTyrSerIleAla-----CystePheAla 49

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C;Sequence: 79 TAAGGCT-----GGTCATCGGGTCCGTACCTGCTAACCTGCTGGCCAG 129

C;Sequence: 34 GlnGlyGlySerGlyTyrCysTyrSerIleAla-----CystePheAla 49

C;Sequence: 19 TGGTGTGGTGTCTGCAACTACACTTCCGATGCAAGGTGAGTCAG 7B

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C;Sequence: 19 TGGTGTGGTGTCTGCAACTACACTTCCGATGCAAGGTGAGTCAG 7B

C;Sequence: 16 CyPherPheLeuglylAsn-----GluasnCysAspIysGluCysLysAlaLysAsn 33

C;Sequence: 79 TAAGGCT-----GGTCATCGGGTCCGTACCTGCTAACCTGCTGGCCAG 129

C;Sequence: 34 GlnGlyGlySerGlyTyrCysTyrSerIleAla-----CystePheAla 49

C;Sequence: 19 TGGTGTGGTGTCTGCAACTACACTTCCGATGCAAGGTGAGTCAG 7B

C;Sequence: 16 CyPherPheLeuglylAsn-----GluasnCysAspIysGluCysLysAlaLysAsn 33

C;Sequence: 79 TAAGGCT-----GGTCATCGGGTCCGTACCTGCTAACCTGCTGGCCAG 129

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C;Sequence: 34 GlnGlyGlySerGlyTyrCysTyrSerIleAla-----CystePheAla 49

C;Sequence: 19 TGGTGTGGTGTCTGCAACTACACTTCCGATGCAAGGTGAGTCAG 7B

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C;Sequence: 79 TAAGGCT-----GGTCATCGGGTCCGTACCTGCTAACCTGCTGGCCAG 129

C;Sequence: 34 GlnGlyGlySerGlyTyrCysTyrSerIleAla-----CystePheAla 49

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C;Sequence: 19 TGGTGTGGTGTCTGCAACTACACTTCCGATGCAAGGTGAGTCAG 7B

C;Sequence: 16 CyPherPheLeuglylAsn-----GluasnCysAspIysGluCysLysAlaLysAsn 33

C;Sequence: 79 TAAGGCT-----GGTCATCGGGTCCGTACCTGCTAACCTGCTGGCCAG 129

C;Sequence: 34 GlnGlyGlySerGlyTyrCysTyrSerIleAla-----CystePheAla 49

C;Sequence: 19 TGGTGTGGTGTCTGCAACTACACTTCCGATGCAAGGTGAGTCAG 7B

C;Sequence: 16 CyPherPheLeuglylAsn-----GluasnCysAspIysGluCysLysAlaLysAsn 33

C;Sequence: 79 TAAGGCT-----GGTCATCGGGTCCGTACCTGCTAACCTGCTGGCCAG 129

C;Sequence: 34 GlnGlyGlySerGlyTyrCysTyrSerIleAla-----CystePheAla 49

C;Sequence: 19 TGGTGTGGTGTCTGCAACTACACTTCCGATGCAAGGTGAGTCAG 7B

C;Sequence: 16 CyPherPheLeuglylAsn-----GluasnCysAspIysGluCysLysAlaLysAsn 33

C;Sequence: 79 TAAGGCT-----GGTCATCGGGTCCGTACCTGCTAACCTGCTGGCCAG 129

C;Sequence: 34 GlnGlyGlySerGlyTyrCysTyrSerIleAla-----CystePheAla 49

C;Sequence: 19 TGGTGTGGTGTCTGCAACTACACTTCCGATGCAAGGTGAGTCAG 7B

C;Sequence: 16 CyPherPheLeuglylAsn-----GluasnCysAspIysGluCysLysAlaLysAsn 33

C;Sequence: 79 TAAGGCT-----GGTCATCGGGTCCGTACCTGCTAACCTGCTGGCCAG 129

C;Sequence: 34 GlnGlyGlySerGlyTyrCysTyrSerIleAla-----CystePheAla 49

C;Sequence: 19 TGGTGTGGTGTCTGCAACTACACTTCCGATGCAAGGTGAGTCAG 7B

C;Sequence: 16 CyPherPheLeuglylAsn-----GluasnCysAspIysGluCysLysAlaLysAsn 33

C;Sequence: 79 TAAGGCT-----GGTCATCGGGTCCGTACCTGCTAACCTGCTGGCCAG 129

C;Sequence: 34 GlnGlyGlySerGlyTyrCysTyrSerIleAla-----CystePheAla 49

RESULTS 6

Species: Leirus quinquestriatus (Egyptian scorpion)

Date: 15-Oct-1982 #sequence_revision 27-Nov-1985 #text_change 28-Aug-1998

Accession: A01749

Author: Kopeyan, C.; Martinez, G.; Rochat, H.

Title: Primary structure of toxin IV of Leirus quinquestriatus

Reference number: A01749

Molecule type: protein

Residues: 1-65 KOP

Note: the source is designated as Leirus quinquestriatus quinquestriatus

Superfamily: scorpion neurotoxin

Keywords: blocked carboxyl end; neurotoxin; sodium channel inhibitor; venom

;13-64,17-37,27-47,27-49 Disulfide bonds: #status predicted

;65/Modified site: blocked carboxyl end (Arg) (probably amidated) #status experimental

Alignment Scores:

| Pred. No.: | Length: | Score: |
|------------|---------|--|
| NTSR4L | 65 | 0.274 |
| Y | 57 | 16 TCCGCGCTGGTGTGAACTACACTCCGATTGCAACGGTAGTGCAAGAGGG 75 |
| b | 30 | AsnCysValtyrHisCysVal-----ProProCysAspGlyLeucysLysysAsn 46 |
| Y | 76 | GCTTACAAAGCTGGTCACTGGGTCTTC----GCTAACGTTGAACTGGTGC 126 |
| Db | 47 | GlyAlaLysSerGlySerGlyPheLeuIleProSerGlyLeuAlaCysTrpCys 65 |

RESULTS 6

Species: Leirus quinquestriatus (Egyptian scorpion)

Date: 15-Oct-1982 #sequence_revision 27-Nov-1985 #text_change 28-Aug-1998

Accession: A01749

Author: Kopeyan, C.; Martinez, G.; Rochat, H.

Title: Primary structure of toxin IV of Leirus quinquestriatus

Reference number: A01749

Molecule type: protein

Residues: 1-65 KOP

Note: the source is designated as Leirus quinquestriatus quinquestriatus

Superfamily: scorpion neurotoxin

Keywords: blocked carboxyl end; neurotoxin; sodium channel inhibitor; venom

;13-64,17-37,27-47,27-49 Disulfide bonds: #status predicted

;65/Modified site: blocked carboxyl end (Arg) (probably amidated) #status experimental

Alignment Scores:

| Pred. No.: | Length: | Score: |
|------------|---------|--|
| NTSR4L | 65 | 0.274 |
| Y | 57 | 16 TCCGCGCTGGTGTGAACTACACTCCGATTGCAACGGTAGTGCAAGAGGG 75 |
| b | 30 | AsnCysValtyrHisCysVal-----ProProCysAspGlyLeucysLysysAsn 46 |
| Y | 76 | GCTTACAAAGCTGGTCACTGGGTCTTC----GCTAACGTTGAACTGGTGC 126 |
| Db | 47 | GlyAlaLysSerGlySerGlyPheLeuIleProSerGlyLeuAlaCysTrpCys 65 |

RESULTS 7

Species: Leirus quinquestriatus (Leirus quinquestriatus)

Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 02-Sep-2000

Accession: B34123

Author: Zlotkin, E.; Fowler, E.; Bitan, M.; Moyer, M.; Adams, M.E.

Title: On the chemistry and action of the depressant insect toxins

Reference number: A31123

Molecule type: protein

Residues: 1-61 <ZL01>

Y

Db

48 TrpCys 49

RESULTS 7

Species: Leirus quinquestriatus (Leirus quinquestriatus)

Date: 06-Jul-1990 #sequence_revision 06-Jul-1990 #text_change 02-Sep-2000

Accession: B34123

Author: Zlotkin, E.; Fowler, E.; Bitan, M.; Moyer, M.; Adams, M.E.

Title: On the chemistry and action of the depressant insect toxins

Reference number: A31123

Molecule type: protein

Residues: 1-61 <ZL01>

Y

Db

48 TrpCys 49

RESULTS 9

Species: Centruroides scutulatus (bark scorpion)

Date: 22-Jun-1981 #sequence_revision 22-Jun-1981 #text_change 31-Mar-2000

Accession: A01752

Author: Babin, D.R.; Watt, D.D.; Goos, S.M.; Mieinek, R.V.

Title: Primary structure of scorpion anti-insect toxins isolated from the venom of Lei

Reference number: S08267

Molecule type: protein

Residues: 1-61 <KOP>

Y

Db

42 PheGlyAsnAla--CysTrpCysCys 49

Biochemistry 30, 4814-4821, 1991
 A;Title: Functional duality and structural uniqueness of depressant insect selective receptor
 A;Reference number: A08526; MUID:91210120; PMID:2029523
 A;Molecule type: protein
 A;Residues: 1-61 <ZLC2>
 A;Cross references: CAS:133300-67-3
 C;Superfamily: scorpion neurotoxin
 C;Keywords: neurotoxin; venom
 F10:6C14-35,21-42,25-44/Disulfide bonds: #status predicted

Alignment Scores:

| Pred. No.: | Length: | Score: |
|------------|---------|--|
| NTSR4L | 65 | 0.368 |
| Y | 76 | 16 TCCGCGCTGGTGTGAACTACACTCCGATTGCAACGGTAGTGCAAGAGGG 75 |
| b | 30 | AsnCysValtyrHisCysVal-----ProProCysAspGlyLeucysLysysAsn 46 |
| Y | 76 | GCTTACAAAGCTGGTCACTGGGTCTTC----GCTAACGTTGAACTGGTGC 126 |
| Db | 47 | GlyAlaLysSerGlySerGlyPheLeuIleProSerGlyLeuAlaCysTrpCys 65 |

RESULTS 8

Species: Neurotoxin Mi4 - lesser Asian scorpion

Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 31-Dec-1993

Accession: JT0020

Author: Volkova, T.M.; Garsia, A.F.; Telezhinskaya, I.N.; Potapenko, N.A.; Grishan, E.V.; Biloog, Khim. 11, 1445-1456, 1985

Title: Study of neurotoxins from the venom of central Asian scorpion *Ritius e-peanus*

Reference number: A94652; MUID:86130759; PMID:409186C

Molecule type: protein

Residues: 1-66 <VOL>

Comment: The venom of this scorpion contains three major polypeptide neurotoxins: Mi4.

Superfamily: scorpion neurotoxin

Keywords: neurotoxin; venom

F12:65,16-36,22-46,26-48/Disulfide bonds: #status predicted

Alignment Scores:

| Pred. No.: | Length: | Score: |
|------------|---------|---|
| NTSR4E | 66 | 0.418 |
| Y | 58 | 16 TCCGCGCTGGTGTGAACTACACTCCGATTGCAACGGTAGTGCAAGAGGG 69 |
| b | 32 | AsnCysValtyrHisCysVal-----CysAsnThrGlySerAsnSerTyrr 28 |
| Y | 70 | AGGGGGSTTACAGGGTGTACTGCT-----GTTCTCTCGTAACGTGAACTG 120 |
| Db | 47 | GlyAsnGlyAlaGluSerGlyTyrrCysGlnTrpLeuGlyLyteGlyLeuAla--Cys 47 |
| Y | 121 | TGGTGC 126 |
| b | 48 | TrpCys 49 |

RESULTS 8

Species: Bark scorpion (tentative sequence)

Date: 22-Jun-1981 #sequence_revision 22-Jun-1981 #text_change 31-Mar-2000

Accession: B34123

Author: Zlotkin, E.; Fowler, E.; Bitan, M.; Moyer, M.; Adams, M.E.

Title: On the chemistry and action of the depressant insect toxins

Reference number: A31123

Molecule type: protein

Residues: 1-61 <ZL01>

Y

Db

42 CysAsnAla--CysTrpCysCys 49

RESULTS 9

Species: Centruroides scutulatus (bark scorpion)

Date: 22-Jun-1981 #sequence_revision 22-Jun-1981 #text_change 31-Mar-2000

Accession: A01752

Author: Babin, D.R.; Watt, D.D.; Goos, S.M.; Mieinek, R.V.

Title: Primary structure of scorpion anti-insect toxins isolated from the venom of Lei

Reference number: S08267

Molecule type: protein

Residues: 1-61 <KOP>

Y

Db

42 PheGlyAsnAla--CysTrpCysCys 49

A;Title: Amino acid sequences of neurotoxic protein variants from the venom of Centruroides vittatus
 A;Reference number: A90358; MUID:75163395; PMID:446085

A;Molecule type: protein

A;Residues: i-65 <DB>

C;Species: scorpion neurotoxin

C;Keywords: neurotoxin; venom

F;12:64;16:41-27:46;29:48//disulfide bonds: #status predicted

C;Accession: C23727
 R;David, R.M.; Krishna, N.R.; Watt, D.J.

A;Title: Characterization of cationic binding sites of neurotoxins from venom of the :

A;Reference number: A23727; MUID:9202384; PMID:1926166

A;Accession: C23727

A;Status: Preliminary

A;Molecule type: protein

A;Residues: 1-59 <DAV>

C;Superfamily: scorpion neurotoxin
 C;Keywords: neurotoxin

C;Accession: C23727

C;Species: scorpion neurotoxin

C;Keywords: neurotoxin

C;Accession: C23727

C;Species: scorpion neurotoxin

C;Keywords: neurotoxin

C;Accession: C23727

C;Species: scorpion neurotoxin

C;Keywords: neurotoxin

C;Accession: C23727

C;Species: scorpion neurotoxin

C;Keywords: neurotoxin

C;Accession: C23727

C;Species: scorpion neurotoxin

C;Keywords: neurotoxin

C;Accession: C23727

C;Species: scorpion neurotoxin

C;Keywords: neurotoxin

C;Accession: C23727

C;Species: scorpion neurotoxin

C;Keywords: neurotoxin

C;Accession: C23727

C;Species: scorpion neurotoxin

C;Keywords: neurotoxin

C;Accession: C23727

C;Species: scorpion neurotoxin

C;Keywords: neurotoxin

C;Accession: C23727

C;Species: scorpion neurotoxin

C;Keywords: neurotoxin

C;Accession: C23727

C;Species: scorpion neurotoxin

C;Keywords: neurotoxin

C;Accession: C23727

C;Species: scorpion neurotoxin

C;Keywords: neurotoxin

C;Accession: C23727

C;Species: scorpion neurotoxin

C;Keywords: neurotoxin

C;Accession: C23727

C;Species: scorpion neurotoxin

C;Keywords: neurotoxin

C;Accession: C23727

C;Species: scorpion neurotoxin

C;Keywords: neurotoxin

C;Accession: C23727

C;Species: scorpion neurotoxin

C;Keywords: neurotoxin

C;Accession: C23727

C;Species: scorpion neurotoxin

C;Keywords: neurotoxin

C;Accession: C23727

C;Species: scorpion neurotoxin

C;Keywords: neurotoxin

C;Accession: C23727

C;Species: scorpion neurotoxin

C;Keywords: neurotoxin

C;Accession: C23727

C;Species: scorpion neurotoxin

C;Keywords: neurotoxin

C;Accession: C23727

C;Species: scorpion neurotoxin

C;Keywords: neurotoxin

C;Accession: C23727

C;Species: scorpion neurotoxin

C;Keywords: neurotoxin

C;Accession: C23727

C;Species: scorpion neurotoxin

C;Keywords: neurotoxin

C;Accession: C23727

C;Species: scorpion neurotoxin

C;Keywords: neurotoxin

RESULT 10

grosscytac precursor - fruit fly (Drosophila melanogaster);

N;Alternate name: cysteine-rich Peptide

C;Species: Drosophila melanogaster

C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 21-Jul-2000

C;Accession: S3824; S3875

A;Reference: Buillet, P.; Michaut, L.; Lagreux, M.; Broekert, W.F.; Hetru, C.; Hoffmann

J. Biol. Chem., 269, 33159-33163, 1994

A;Title: Insect immunity: Septic injury of Drosophila induces the synthesis of a potent

A;Reference number: A55824; MUID:95105209; PMID:7865466

A;Accession: A55824

A;Molecule type: protein

A;Residues: 1-70 <FEH>

A;Cross references: EMBL:X75595; NCBI:9414661; PID:3414662

A;Note: the mature peptide sequence was confirmed by peptide sequencing

C;Comment: The exact site of signal peptide cleavage and the requirement for a

C;Genetics:

A;Gene: FlyBase:trs

A;Cross references: FlyBase:FBgn0010391

C;Keywords: disulfide bond; extracellular; protein

F;27-70/Product: drosomycin #status experimental <NAT>

A;Cross references: F17C04.1

A;Gene: FBgn0010391

A;Cross references: FBgn0010391

C;Keywords: disulfide bond; extracellular; protein

F;27-70/Product: drosomycin #status experimental <NAT>

A;Cross references: F17C04.1

A;Gene: FBgn0010391

A;Cross references: FBgn0010391

C;Keywords: disulfide bond; extracellular; protein

F;27-70/Product: drosomycin #status experimental <NAT>

A;Cross references: F17C04.1

A;Gene: FBgn0010391

A;Cross references: FBgn0010391

C;Keywords: disulfide bond; extracellular; protein

F;27-70/Product: drosomycin #status experimental <NAT>

A;Cross references: F17C04.1

A;Gene: FBgn0010391

A;Cross references: FBgn0010391

C;Keywords: disulfide bond; extracellular; protein

F;27-70/Product: drosomycin #status experimental <NAT>

A;Cross references: F17C04.1

A;Gene: FBgn0010391

A;Cross references: FBgn0010391

C;Keywords: disulfide bond; extracellular; protein

F;27-70/Product: drosomycin #status experimental <NAT>

A;Cross references: F17C04.1

A;Gene: FBgn0010391

A;Cross references: FBgn0010391

C;Keywords: disulfide bond; extracellular; protein

F;27-70/Product: drosomycin #status experimental <NAT>

A;Cross references: F17C04.1

A;Gene: FBgn0010391

A;Cross references: FBgn0010391

C;Keywords: disulfide bond; extracellular; protein

F;27-70/Product: drosomycin #status experimental <NAT>

A;Cross references: F17C04.1

A;Gene: FBgn0010391

A;Cross references: FBgn0010391

C;Keywords: disulfide bond; extracellular; protein

F;27-70/Product: drosomycin #status experimental <NAT>

A;Cross references: F17C04.1

A;Gene: FBgn0010391

A;Cross references: FBgn0010391

C;Keywords: disulfide bond; extracellular; protein

F;27-70/Product: drosomycin #status experimental <NAT>

A;Cross references: F17C04.1

A;Gene: FBgn0010391

A;Cross references: FBgn0010391

C;Keywords: disulfide bond; extracellular; protein

F;27-70/Product: drosomycin #status experimental <NAT>

A;Cross references: F17C04.1

A;Gene: FBgn0010391

A;Cross references: FBgn0010391

C;Keywords: disulfide bond; extracellular; protein

F;27-70/Product: drosomycin #status experimental <NAT>

A;Cross references: F17C04.1

A;Gene: FBgn0010391

A;Cross references: FBgn0010391

C;Keywords: disulfide bond; extracellular; protein

F;27-70/Product: drosomycin #status experimental <NAT>

A;Cross references: F17C04.1

A;Gene: FBgn0010391

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C;Keywords: disulfide bond; extracellular; protein

F;27-70/Product: drosomycin #status experimental <NAT>

A;Cross references: F17C04.1

A;Gene: FBgn0010391

A;Cross references: FBgn0010391

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F;27-70/Product: drosomycin #status experimental <NAT>

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A;Gene: FBgn0010391

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C;Keywords: disulfide bond; extracellular; protein

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A;Gene: FBgn0010391

A;Cross references: FBgn0010391

C;Keywords: disulfide bond; extracellular; protein

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A;Gene: FBgn0010391

A;Cross references: FBgn0010391

C;Keywords: disulfide bond; extracellular; protein

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F;27-70/Product: drosomycin #status experimental <NAT>

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C;Keywords: disulfide bond; extracellular; protein

F;27-70/Product: drosomycin #status experimental <NAT>

A;Cross references: F17C04.1

A;Gene: FBgn0010391

A;Cross references: FBgn0010391

C;Keywords: disulfide bond; extracellular; protein

F;27-70/Product: drosomycin #status experimental <NAT>

A;Cross references: F17C04.1

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A;Cross references: FBgn0010391

C;Keywords: disulfide bond; extracellular; protein

F;27-70/Product: drosomycin #status experimental <NAT>

A;Cross references: F17C04.1

A;Gene: FBgn0010391

A;Cross references: FBgn0010391

C;Keywords: disulfide bond; extracellular; protein

F;27-70/Product: drosomycin #status experimental <NAT>

A;Cross references: F17C04.1

A;Gene: FBgn0010391

A;Cross references: FBgn0010391

C;Keywords: disulfide bond; extracellular; protein

F;27-70/Product: drosomycin #status experimental <NAT>

A;Cross references: F17C04.1

A;Gene: FBgn0010391

A;Cross references: FBgn0010391

C;Keywords: disulfide bond; extracellular; protein

F;27-70/Product: drosomycin #status experimental <NAT>

A;Cross references: F17C04.1

A;Gene: FBgn0010391

A;Cross references: FBgn0010391

C;Keywords: disulfide bond; extracellular; protein

F;27-70/Product: drosomycin #status experimental <NAT>

A;Cross references: F17C04.1

A;Reference number: A01741; MUID:78191225; PMID:658402
A;Note: L. Q. Quinquestriatus
A;Accession: A01741
A;Molecule type: protein
A;Residues: 1-64
C;Superfamily: scorpion neurotoxin
C;Keywords: blocked carboxyl end; neurotoxin; venom
F=164/Modified site: blocked carboxyl end (Asn) (probably amidated); #status experimental:
Alignment Scores:
pred. No.: 0.981 Length: 64
Score: 73.00 Matches: 12
Percent Similarity: 60.71% Conservative: 5
Best Local Similarity: 42.86% Mismatches: 7
Query Match: 27.34% Indels: 4
QB: 1 Gaps: 2
JS-09-673-274B-2_COPY_1_132 (1-132) x NTSR5L (1-64);
Db 42 TyrglyAsnAla--Cy6TrpCys 48
RESULT 14
NSR5C
C;Species: Centruroides sculputratus (bark scorpion)
C;Date: 15-Oct-1982 #sequence revision 15-Oct-1982 #text_change 23-Aug-1996
R;Babin, D.R.; Watt, D.D.; Goob, S.M.; Melenek, R.V.
Arch. Biochem. Biophys. 164: 694-706, 1974
A;Title: Amino acid sequences of neurotoxic protein variants from the venom of Centruroides sculputratus
A;Accession: A94470
A;Molecule type: protein
A;Residues: 1-24, NTC, '28-63, 'CS, 'BAB
R;Bhown, A.; Mole, J.; Toxicon 20, 1-7, 1982
A;Unpublished results, cited by Fontecilla-Camps, J.C., et al., Toxicon 20, 1-7, 1982
A;Accession: A94470
A;Molecule type: protein
A;Residues: 1-65 -BHO>
R;Fontecilla-Camps, J.C.; Almassy, R.J.; Suddath, F.L.; Bigg, C.E.
A;Title: The three-dimensional structure of scorpion neurotoxins.
A;Reference number: A9314; MUID:82200153; PMID:7080025
A;Contents: annotation, X-ray crystallography, 1.8 angstroms; disulfide bonds
A;Note: X-ray crystallographic studies were based on the revised sequence shown
C;Superfamily: scorpion neurotoxin
C;Keywords: venom
F=12-65/16-41,25-46,29-48/Disulfide bonds: #status experimental

Db 32 LysAsnGlnGlyGlySertyrGlyTyrCystyRiaApheAla-----Cy6TrpCys 48
Qy 127 GAG 129
Db 49 Glu 49

RESULT 15
JNC610
Na+-channel-blocking toxin (clone cngtIII) precursor - scorpion (Centruroides noxius):
C;Species: Centruroides noxius
C;Date: 03-Feb-1994 #sequence_revision: 03-Feb-1994 #text_change 16-Jul-1999
C;Accession: JN0670
R;Beerruti, B.; Vazquez, A.; Garcia, C.; Corona, M.; Bolivar, F.; Possani, L.D.
Gene 128, 165-171, 1993
A;Title: Cloning and characterization of cDNAs that code for Na+-channel blocking toxin
A;Reference number: JN0669; MUID:93242953; PMID:8390386
A;Accession: JN0670
A;Molecule type: mRNA
A;Residues: 1-87 <REC>
A;Cross-references: GB-L25061; NID:9304566; PID:AAA28286_1; PID:9104569
A;Experimental source: venom gland
C;Superfamily: scorpion neurotoxin
C;Keywords: toxin
F=1-19/Doain: signal sequence #status predicted <SIG>
F=2C-87/Product: Na+-channel-blocking toxin (clone cngtIII); #status predicted <NAAT>
Alignment Scores:
Pred. No.: 1.88 Length: 87
Score: 70.50 Matches: 15
Percent Similarity: 48.72% Conservative: 4
Best Local Similarity: 38.46% Mismatches: 1
Query Match: 26.40% Indels: 3
DB: 2 Gaps: 3
JS-09-673-274B-2_COPY_1_132 (1-132) x CN0670 (1-87)
Qy 19 TGCCTGGGTGGTGTGAACACTTCACTTGAGTGCAGAACGGTGGTGGAACTGAGTGCAGAGGAGGTT
Db 35 CysPheTrpIleGlyLysAsn-----GluGlyCysAspLysGluCysAspAlysAsp: 52
Qy 79 TACAAGGT-----3GTCACTGGGTCCCTTCGCTTAACGTGAACTGCTGGCGAG 126
Db 53 GluGlyGlySertyrGlyTyrCystyRiaAphe-----Glyc6TrpCysGlu 68

Search completed: October 16, 2003, 17:11:59
Job time : 17.2259 secs

GenCore version 5.1.6
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DB nucleic - protein search, using frame_plus_n2p model

run on: October 16, 2003, 17:06:37 : Search time 39.0299 seconds
 (without alignments)

title: US-09-673-274B-2_COPY_1_132
 perfect score: 267

sequence: 1 gataaagtatcgttccgt.....tgaaactgtgtgtgcgact 132
 scoring table: BLOSUM62
 Xgapext 10.0 , Ygapext 0.5
 Ygapop 10.0 , Ygapext 0.5
 Fgapop 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 1661050

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%, Maximum Match 100%
 Listing first 45 summaries

Command line parameters:
 MODEL-frame+ n2p model , DEV=xlp
 Q= /cgn1/1/uspto/spool/us06732/4/runat_16102003_170627_2545/app/query.fasta_1_654
 DB=SPTREMBL
 -DBFORMAT=fastan
 -MINMATCH=0.1
 -LOOPEXT=0
 -UNITS=bits
 -START=1
 -END=1
 -DOCALIGN=200
 -THR SCORE=pct
 -THR MAX=100
 -TRANS=human40_cdi
 -LIST=45
 -NORMEXT
 -HEAPSIZE=500
 -MINLEN=100
 -MAXLEN=200000000
 -OUTFILE=uspto
 -USER=US096732/4/runat_1610627_2545
 -NCPU=6
 -ICPU=3
 -NO MMAP
 -LARGEQUERY
 -NEG SCORES=0
 -WAIT -DSBLOCK=100 -LONGLOG
 -DEV TIMEOUT=120 -WARN TIMEOUT=10 -XGAPPOP=10 -XGAPEXT=0.5 -FGAPPOP=6
 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELPOP=6 -DELEXT=7

Database :

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_rvirus:*
- 16: sp_bacteriophage:*
- 17: sp_archeap:*

SPTREMBL 23:*

SEQUENCE FROM N.A.

PRELIMINARY:

PRT: 65 AA.

RESULT :

ID Q17231 PRELIMINARY; PRT: 65 AA.
 AC ID Q17231
 DT 01-NOV-1996 ("TREMBL"; 01, Created);
 DT 01-MAR-2003 ("TREMBL"; 01, Last sequence update);
 DE Insect toxin 2.

IT2.

OS Mesobuthus martensii (Manchurian scorpion); (Ruthus martensis);
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
 OC Buthidae; Mesobuthus.

NCBI_TaxID=34649;

(1)

SEQUENCE FROM N.A.

RC Tissue=Teision;
 RA Zhu X., Zhang T., Zhu Y.; Cloning and sequencing of two depressant insect selective neurotoxin cDNAs from Ruthus martensii Karsch.;
 RT Kexue Tongbao 41:1381-1391.(1996).

CC ! SIMILARITY LOCATION: SECRETED (BY SIMILARITY).
 CC ! BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY.

DR HSSP: P0194; 2SN3.

DR InterPro: IPR003614; Knot1.

SUMMARIES

| Result No. | Score | Match Length | DB ID | Description |
|------------|-------|--------------|-------|-------------------|
| 1 | 84.5 | 31.6 | 65 5 | Q17231 mesobuthus |

Pre. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| | | | | |
|---|---|---------------|----------|---------------------------------------|
| FT | SIGNAL | 1 | 21 | POTENTIAL. |
| FT | CHAIN | 22 | 82 | DEPRESSANT INSECT NEUROTOXIN BMK ITB. |
| SQ | SEQUENCE | 85 AA; | 9330 MW; | 80CD3914956DE8C CRC64; |
| Alignment Scores: | | | | |
| Pred. No.: | 0.0268 | Length: | 85 | |
| Score: | 55.26% | Matches: | 15 | |
| Percent Similarity: | 55.26% | Conservative: | 6 | |
| Best Local Similarity: | 39.47% | Mismatches: | 12 | |
| Query Match: | 30.52% | Indels: | 5 | |
| DB: | 5 | Gaps: | 2. | |
| RESULT 5 | | | | |
| ID Q9XY87 | PRELIMINARY; | PRT; | 85 AA. | |
| AC Q9XY87; | | | | |
| DT 01-NOV-1999 (TREMBLrel 12, Created) | | | | |
| DT 01-NOV-1999 (TREMBLrel 12, Last sequence update) | | | | |
| DT 01-MAR-2003 (TREMBLrel 23, Last annotation update) | | | | |
| Neurotoxin APP precursor. | | | | |
| CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY). | | | | |
| Mesobuthus martensii (Manchurian scorpion) (Buthus martensii), Eukaryota; Metazoa; Arthropoda; Chelicerata; Scorpiones; Arachnida; Mesobuthus. | | | | |
| OC NCBITaxID=34649; | | | | |
| RN [2] | | | | |
| RP SEQUENCE FROM N.A. | | | | |
| RA Liu Z., Chi C., Wu X.; | | | | |
| RA Liu Z., Chi C., Wu X.; | | | | |
| RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases. | | | | |
| CC -!- SIMILARITY: BELONGS TO THE ALPHA/BETA-SCORPION TOXIN FAMILY. | | | | |
| DR AY030782; AAW09397; . | | | | |
| DR InterPro: IPR003614; Kro1 | | | | |
| DR InterPro: IPR002C61; ScorpLoc_toxins.. | | | | |
| DR Pfam: PF00537; toxin_3; | | | | |
| DR ProDom; PD000908; Scorpion_ToxinL; 1. | | | | |
| DR SMART; SM00505; Kro1; 1. | | | | |
| DR SMART; SM00505; Kro1; 1. | | | | |
| FT SIGNAL. | | | | |
| SQ SEQUENCE 85 AA; 92:4 MR; 6CP56TC36012CC1A CRC64; | | | | |
| Alignment Scores: | | | | |
| Pred. No.: | 0.0366 | Length: | 85 | |
| Score: | 80.56% | Matches: | 15 | |
| Percent Similarity: | 52.53% | Conservative: | 5 | |
| Best Local Similarity: | 39.47% | Mismatches: | 13 | |
| Query Match: | 30.15% | Indels: | 5 | |
| DB: | 5 | Gaps: | 2 | |
| RESULT 7 | | | | |
| ID P82761 | PRELIMINARY; | PRT; | 91 AA. | |
| AC P82761; | | | | |
| DT 01-OCT-2002 (TREMBLrel 22, Created) | | | | |
| DT 01-OCT-2002 (TREMBLrel 22, Last sequence update) | | | | |
| DT 01-OCT-2002 (TREMBLrel 22, Last annotation update) | | | | |
| DR Hypothetical protein LCR16 precursor. | | | | |
| GN LCR46 | | | | |
| Arabidopsis thaliana (mouse-ear cress). | | | | |
| Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; | | | | |
| Spermato phyta; Magnoliophyta; Eudicotyledons; Core eudicots; Rosidae; | | | | |
| euroids II; Brassicales; Brassicaceae; Arabidopsis. | | | | |
| RN [1]; | | | | |
| RP SEQUENCE FROM N.A. | | | | |
| RC STRAIN=Cv. Columbia; | | | | |
| RX MEDLINE=939745; PubMed=10473850; | | | | |
| RA Kaneko T., Katoch T., Sato S., Nakatara Y., Asamizu E., Kotani H., Miyajima N., Tabata S.; | | | | |
| RT "Structural analysis of Arabidopsis thaliana chromosome 5. IX. Sequence features of the regions of 1,011,550 bp covered by seventeen P1 and TAC clones." | | | | |
| RT DNA Res. 6:183-295(1999). | | | | |
| RN [2] | | | | |
| RP IDENTIFICATION. | | | | |
| RX PubMed=11437247; | | | | |
| RA Vanoostruys V., Miege C., Dumas C., Cock J.M.; | | | | |
| RT "Two large Arabidopsis thaliana gene families are homologous to the Brassica gene superfamily that encodes pollen coat proteins and the | | | | |
| RESULT 6 | | | | |
| ID Q8T3TO | PRELIMINARY; | PRT; | 85 AA. | |
| DB | 50 GlyAlaSerTyrGlyTyrCysTrpThrTrp--GlyLeuAlaCysTrpCysGln 66 | | | |

| | | | | |
|---|---|------|---------|--|
| RT | "The genome sequence of <i>Drosophila melanogaster</i> ."; | | | |
| RL | Science 287:2185-2195 (2000); | | | |
| RN | [2] | | | |
| RP | SEQUENCE ERCM N.A. | | | |
| RC | S7RA-N-Berkley/ | | | |
| RA | Stableton M., Brokstein P., Hong L., Agbayani A., Carlson J., Frise E., George M., Chavez C., Dorsett V., Dreske C., Farfan D., Friesenfeld C., Krommiller B., Li P., Liac G., | | | |
| RA | Miranda A., Mangail C.J., Narro J., Pacie J., Paragas V., Park S., Peinker S., Phouanavong S., War K., Yu C., Lewis S.E., Rubin G.M., Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases. | | | |
| RA | EMBL; AE034477; AAF67757; -; | | | |
| DR | FlyBase; FBgn0035434; CG10812; | | | |
| DR | InterPro; IPR002118; Gamma-thionine; | | | |
| DR | ProdB; P002594; Proline; | | | |
| CR | HSSP; P4164; 1MYN. | | | |
| DR | Protein; P005622; 1; | | | |
| SQ | SEQUENCE 69 AA; 7656 MW; 7255EF8B1DCC6F7 CRC64; | | | |
| RESULT 13 | | | | |
| Q9YUA7 | PRELIMINARY; | PRT; | 85 AA. | |
| ID | Q9YUA7; | | | |
| AC | Q9YUA7; | | | |
| Length: | 84 | | | |
| Score: | 0.236 | | | |
| Percent Similarity: | 74.50 | | | |
| Best Local Similarity: | 48.72% | | | |
| Query Match: | 35.90% | | | |
| DB: | 27.90% | | | |
| US-09-673-274B-2_CCPY_1_132 (1-132) × Q8WRY4 (1-84) | | | | |
| Qy | 19 TCGGTGGGGTGGCTGACTACATTCGGAT-----TGCAACGGTAGTGAAAGCG 72 | | | |
| Db | 31 CysThrLeuIaCysIleAspLysThrGlyAspLysAspArgAsnCysLys 50 | | | |
| Qy | 73 AGGGTTACAGGGTGGTACTGGCGTTCTTCGTAACGTGAAGCTGAACTGGTGCAG 129 | | | |
| Db | 51 GluGlyIleSerPheGlyHisCysSerTyrSerAla-----CysTrpCysLys 66 | | | |
| RESULT 14 | | | | |
| Q9YVR3 | PRELIMINARY; | PRT; | 106 AA. | |
| ID | Q9YVR3 | | | |
| AC | Q9YVR3 | | | |
| Length: | 85 | | | |
| Score: | 0.278 | | | |
| Percent Similarity: | 74.00 | | | |
| Best Local Similarity: | 64.29% | | | |
| Query Match: | 42.86% | | | |
| DB: | 27.72% | | | |
| US-09-673-274B-2_CCPY_1_132 (1-132) × Q9GUAT (1-85) | | | | |
| Qy | 52 TGAAACGGTGAGTCAAAGGGGTTACAGGGTGACTGGTGC-----CGTTCC 102 | | | |
| Db | 41 CysAspAspGlucLysLysGlyAlaIuserGlyItyrCysGlnrpAlaGlyval 60 | | | |
| Qy | 103 TTGGCTAACGTGAACTGGTGC 126 | | | |
| Db | 61 TyrGlyAsnAla---CysTrpCys 67 | | | |
| RESULT 15 | | | | |
| Q9YVR3 | PRELIMINARY; | PRT; | 106 AA. | |
| ID | Q9YVR3 | | | |
| AC | Q9YVR3 | | | |
| Length: | 85 | | | |
| Score: | 0.278 | | | |
| Percent Similarity: | 74.00 | | | |
| Best Local Similarity: | 64.29% | | | |
| Query Match: | 42.86% | | | |
| DB: | 27.72% | | | |
| US-09-673-274B-2_CCPY_1_132 (1-132) × Q9GUAT (1-85) | | | | |
| Qy | 52 TGAAACGGTGAGTCAAAGGGGTTACAGGGTGACTGGTGC-----CGTTCC 102 | | | |
| Db | 41 CysAspAspGlucLysLysGlyAlaIuserGlyItyrCysGlnrpAlaGlyval 60 | | | |
| Qy | 103 TTGGCTAACGTGAACTGGTGC 126 | | | |
| Db | 61 TyrGlyAsnAla---CysTrpCys 67 | | | |
| RESULT 16 | | | | |
| Q9YVR3 | PRELIMINARY; | PRT; | 106 AA. | |
| ID | Q9YVR3 | | | |
| AC | Q9YVR3 | | | |
| Length: | 85 | | | |
| Score: | 0.278 | | | |
| Percent Similarity: | 74.00 | | | |
| Best Local Similarity: | 64.29% | | | |
| Query Match: | 42.86% | | | |
| DB: | 27.72% | | | |
| US-09-673-274B-2_CCPY_1_132 (1-132) × Q9GUAT (1-85) | | | | |
| Qy | 52 TGAAACGGTGAGTCAAAGGGGTTACAGGGTGACTGGTGC-----CGTTCC 102 | | | |
| Db | 41 CysAspAspGlucLysLysGlyAlaIuserGlyItyrCysGlnrpAlaGlyval 60 | | | |
| Qy | 103 TTGGCTAACGTGAACTGGTGC 126 | | | |
| Db | 61 TyrGlyAsnAla---CysTrpCys 67 | | | |
| RESULT 17 | | | | |
| Q9YVR3 | PRELIMINARY; | PRT; | 106 AA. | |
| ID | Q9YVR3 | | | |
| AC | Q9YVR3 | | | |
| Length: | 85 | | | |
| Score: | 0.278 | | | |
| Percent Similarity: | 74.00 | | | |
| Best Local Similarity: | 64.29% | | | |
| Query Match: | 42.86% | | | |
| DB: | 27.72% | | | |
| US-09-673-274B-2_CCPY_1_132 (1-132) × Q9GUAT (1-85) | | | | |
| Qy | 52 TGAAACGGTGAGTCAAAGGGGTTACAGGGTGACTGGTGC-----CGTTCC 102 | | | |
| Db | 41 CysAspAspGlucLysLysGlyAlaIuserGlyItyrCysGlnrpAlaGlyval 60 | | | |
| Qy | 103 TTGGCTAACGTGAACTGGTGC 126 | | | |
| Db | 61 TyrGlyAsnAla---CysTrpCys 67 | | | |
| RESULT 18 | | | | |
| Q9YVR3 | PRELIMINARY; | PRT; | 106 AA. | |
| ID | Q9YVR3 | | | |
| AC | Q9YVR3 | | | |
| Length: | 85 | | | |
| Score: | 0.278 | | | |
| Percent Similarity: | 74.00 | | | |
| Best Local Similarity: | 64.29% | | | |
| Query Match: | 42.86% | | | |
| DB: | 27.72% | | | |
| US-09-673-274B-2_CCPY_1_132 (1-132) × Q9GUAT (1-85) | | | | |
| Qy | 52 TGAAACGGTGAGTCAAAGGGGTTACAGGGTGACTGGTGC-----CGTTCC 102 | | | |
| Db | 41 CysAspAspGlucLysLysGlyAlaIuserGlyItyrCysGlnrpAlaGlyval 60 | | | |
| Qy | 103 TTGGCTAACGTGAACTGGTGC 126 | | | |
| Db | 61 TyrGlyAsnAla---CysTrpCys 67 | | | |
| RESULT 19 | | | | |
| Q9YVR3 | PRELIMINARY; | PRT; | 106 AA. | |
| ID | Q9YVR3 | | | |
| AC | Q9YVR3 | | | |
| Length: | 85 | | | |
| Score: | 0.278 | | | |
| Percent Similarity: | 74.00 | | | |
| Best Local Similarity: | 64.29% | | | |
| Query Match: | 42.86% | | | |
| DB: | 27.72% | | | |
| US-09-673-274B-2_CCPY_1_132 (1-132) × Q9GUAT (1-85) | | | | |
| Qy | 52 TGAAACGGTGAGTCAAAGGGGTTACAGGGTGACTGGTGC-----CGTTCC 102 | | | |
| Db | 41 CysAspAspGlucLysLysGlyAlaIuserGlyItyrCysGlnrpAlaGlyval 60 | | | |
| Qy | 103 TTGGCTAACGTGAACTGGTGC 126 | | | |
| Db | 61 TyrGlyAsnAla---CysTrpCys 67 | | | |
| RESULT 20 | | | | |
| Q9YVR3 | PRELIMINARY; | PRT; | 106 AA. | |
| ID | Q9YVR3 | | | |
| AC | Q9YVR3 | | | |
| Length: | 85 | | | |
| Score: | 0.278 | | | |
| Percent Similarity: | 74.00 | | | |
| Best Local Similarity: | 64.29% | | | |
| Query Match: | 42.86% | | | |
| DB: | 27.72% | | | |
| US-09-673-274B-2_CCPY_1_132 (1-132) × Q9GUAT (1-85) | | | | |
| Qy | 52 TGAAACGGTGAGTCAAAGGGGTTACAGGGTGACTGGTGC-----CGTTCC 102 | | | |
| Db | 41 CysAspAspGlucLysLysGlyAlaIuserGlyItyrCysGlnrpAlaGlyval 60 | | | |
| Qy | 103 TTGGCTAACGTGAACTGGTGC 126 | | | |
| Db | 61 TyrGlyAsnAla---CysTrpCys 67 | | | |
| RESULT 21 | | | | |
| Q9YVR3 | PRELIMINARY; | PRT; | 106 AA. | |
| ID | Q9YVR3 | | | |
| AC | Q9YVR3 | | | |
| Length: | 85 | | | |
| Score: | 0.278 | | | |
| Percent Similarity: | 74.00 | | | |
| Best Local Similarity: | 64.29% | | | |
| Query Match: | 42.86% | | | |
| DB: | 27.72% | | | |
| US-09-673-274B-2_CCPY_1_132 (1-132) × Q9GUAT (1-85) | | | | |
| Qy | 52 TGAAACGGTGAGTCAAAGGGGTTACAGGGTGACTGGTGC-----CGTTCC 102 | | | |
| Db | 41 CysAspAspGlucLysLysGlyAlaIuserGlyItyrCysGlnrpAlaGlyval 60 | | | |
| Qy | 103 TTGGCTAACGTGAACTGGTGC 126 | | | |
| Db | 61 TyrGlyAsnAla---CysTrpCys 67 | | | |
| RESULT 22 | | | | |
| Q9YVR3 | PRELIMINARY; | PRT; | 106 AA. | |
| ID | Q9YVR3 | | | |
| AC | Q9YVR3 | | | |
| Length: | 85 | | | |
| Score: | 0.278 | | | |
| Percent Similarity: | 74.00 | | | |
| Best Local Similarity: | 64.29% | | | |
| Query Match: | 42.86% | | | |
| DB: | 27.72% | | | |
| US-09-673-274B-2_CCPY_1_132 (1-132) × Q9GUAT (1-85) | | | | |
| Qy | 52 TGAAACGGTGAGTCAAAGGGGTTACAGGGTGACTGGTGC-----CGTTCC 102 | | | |
| Db | 41 CysAspAspGlucLysLysGlyAlaIuserGlyItyrCysGlnrpAlaGlyval 60 | | | |
| Qy | 103 TTGGCTAACGTGAACTGGTGC 126 | | | |
| Db | 61 TyrGlyAsnAla---CysTrpCys 67 | | | |
| RESULT 23 | | | | |
| Q9YVR3 | PRELIMINARY; | PRT; | 106 AA. | |
| ID | Q9YVR3 | | | |
| AC | Q9YVR3 | | | |
| Length: | 85 | | | |
| Score: | 0.278 | | | |
| Percent Similarity: | 74.00 | | | |
| Best Local Similarity: | 64.29% | | | |
| Query Match: | 42.86% | | | |
| DB: | 27.72% | | | |
| US-09-673-274B-2_CCPY_1_132 (1-132) × Q9GUAT (1-85) | | | | |
| Qy | 52 TGAAACGGTGAGTCAAAGGGGTTACAGGGTGACTGGTGC-----CGTTCC 102 | | | |
| Db | 41 CysAspAspGlucLysLysGlyAlaIuserGlyItyrCysGlnrpAlaGlyval 60 | | | |
| Qy | 103 TTGGCTAACGTGAACTGGTGC 126 | | | |
| Db | 61 TyrGlyAsnAla---CysTrpCys 67 | | | |
| RESULT 24 | | | | |
| Q9YVR3 | PRELIMINARY; | PRT; | 106 AA. | |
| ID | Q9YVR3 | | | |
| AC | Q9YVR3 | | | |
| Length: | 85 | | | |
| Score: | 0.278 | | | |
| Percent Similarity: | 74.00 | | | |
| Best Local Similarity: | 64.29% | | | |
| Query Match: | 42.86% | | | |
| DB: | 27.72% | | | |
| US-09-673-274B-2_CCPY_1_132 (1-132) × Q9GUAT (1-85) | | | | |
| Qy | 52 TGAAACGGTGAGTCAAAGGGGTTACAGGGTGACTGGTGC-----CGTTCC 102 | | | |
| Db | 41 CysAspAspGlucLysLysGlyAlaIuserGlyItyrCysGlnrpAlaGlyval 60 | | | |
| Qy | 103 TTGGCTAACGTGAACTGGTGC 126 | | | |
| Db | 61 TyrGlyAsnAla---CysTrpCys 67 | | | |
| RESULT 25 | | | | |
| Q9YVR3 | PRELIMINARY; | PRT; | 106 AA. | |
| ID | Q9YVR3 | | | |
| AC | Q9YVR3 | | | |
| Length: | 85 | | | |
| Score: | 0.278 | | | |
| Percent Similarity: | 74.00 | | | |
| Best Local Similarity: | 64.29% | | | |
| Query Match: | 42.86% | | | |
| DB: | 27.72% | | | |
| US-09-673-274B-2_CCPY_1_132 (1-132) × Q9GUAT (1-85) | | | | |
| Qy | 52 TGAAACGGTGAGTCAAAGGGGTTACAGGGTGACTGGTGC-----CGTTCC 102 | | | |
| Db | 41 CysAspAspGlucLysLysGlyAlaIuserGlyItyrCysGlnrpAlaGlyval 60 | | | |
| Qy | 103 TTGGCTAACGTGAACTGGTGC 126 | | | |
| Db | 61 TyrGlyAsnAla---CysTrpCys 67 | | | |
| RESULT 26 | | | | |
| Q9YVR3 | PRELIMINARY; | PRT; | 106 AA. | |
| ID | Q9YVR3 | | | |
| AC | Q9YVR3 | | | |
| Length: | 85 | | | |
| Score: | 0.278 | | | |
| Percent Similarity: | 74.00 | | | |
| Best Local Similarity: | 64.29% | | | |
| Query Match: | 42.86% | | | |
| DB: | 27.72% | | | |
| US-09-673-274B-2_CCPY_1_132 (1-132) × Q9GUAT (1-85) | | | | |
| Qy | 52 TGAAACGGTGAGTCAAAGGGGTTACAGGGTGACTGGTGC-----CGTTCC 102 | | | |
| Db | 41 CysAspAspGlucLysLysGlyAlaIuserGlyItyrCysGlnrpAlaGlyval 60 | | | |
| Qy | 103 TTGGCTAACGTGAACTGGTGC 126 | | | |
| Db | 61 TyrGlyAsnAla---CysTrpCys 67 | | | |
| RESULT 27 | | | | |
| Q9YVR3 | PRELIMINARY; | PRT; | 106 AA. | |
| ID | Q9YVR3 | | | |
| AC | Q9YVR3 | | | |
| Length: | 85 | | | |
| Score: | 0.278 | | | |
| Percent Similarity: | 74.00 | | | |
| Best Local Similarity: | 64.29% | | | |
| Query Match: | 42.86% | | | |
| DB: | 27.72% | | | |
| US-09-673-274B-2_CCPY_1_132 (1-132) × Q9GUAT (1-85) | | | | |
| Qy | 52 TGAAACGGTGAGTCAAAGGGGTTACAGGGTGACTGGTGC-----CGTTCC 102 | | | |
| Db | 41 CysAspAspGlucLysLysGlyAlaIuserGlyItyrCysGlnrpAlaGlyval 60 | | | |
| Qy | 103 TTGGCTAACGTGAACTGGTGC 126 | | | |
| Db | 61 TyrGlyAsnAla---CysTrpCys 67 | | | |
| RESULT 28 | | | | |
| Q9YVR3 | PRELIMINARY; | PRT; | 106 AA. | |
| ID | Q9YVR3 | | | |
| AC | Q9YVR3 | | | |
| Length: | 85 | | | |
| Score: | 0.278 | | | |
| Percent Similarity: | 74.00 | | | |
| Best Local Similarity: | 64.29% | | | |
| Query Match: | 42.86% | | | |
| DB: | 27.72% | | | |
| US-09-673-274B-2_CCPY_1_132 (1-132) × Q9GUAT (1-85) | | | | |
| Qy | 52 TGAAACGGTGAGTCAAAGGGGTTACAGGGTGACTGGTGC-----CGTTCC 102 | | | |
| Db | 41 CysAspAspGlucLysLysGlyAlaIuserGlyItyrCysGlnrpAlaGlyval 60 | | | |
| Qy | 103 TTGGCTAACGTGAACTGGTGC 126 | | | |
| Db | 61 TyrGlyAsnAla---CysTrpCys 67 | | | |
| RESULT 29 | | | | |

Q1-MAR-2003 (TREMBLrel. 23, Last annotation update)
 CG30813 protein
 CG32279 OR CG10813.
 Drosophila melanogaster (Fruit fly).

Drosophila: Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Dipteroidea; Drosophilidae; Drosophila.

NCBI TaxID=7227;

[1]

RN

RP

SEQUENCE N.A.

STRAIN:BERKELEY

MEDLINE=20196006; PubMed=10731122;

QY

61 GAGTCGAAGGGGGTTACACAGGGTCACTGGGTCTCTCGTAACGTAACCTGC 120

DB

84 LieCysLySGLuGluGlyH:sileSerGlyHscysser----ProSerLeuLysysr 10:

DC

TGGTGCAG 129

QY

121 TGGTGCAG 129

DB

102 TrpCysGlu 134

RESULT 15

Q95P69

PRELIMINARY;

ID Q95P69

PRT: 85 AA.

AC Q95P69;

DT 01-DEC-2001 (TREMBLEl. 12, Created)

DT 01-DEC-2001 (TREMBLEl. 12, Last sequence update)

DT 01-MAR-2003 (TREMBLEl. 23, Last annotation update)

DT "Public sodium channel; toxin 3MKT"

DS Mesobuthus martensii (Scorpion) (Buthus martensii)

OC Eukaryota; Merazoa; Arthropoda; Cheliceraata; Arachnida; Scorpiones;

OC Buthidae; Buthidae; Mesobuthus.

OC NCBI TaxID=34649;

RN [1] -

RN SEQUENCE FROM N.A.

RN STRAIN=10; TISSUE=Venom gland;

RN RC Q95P69; PubMed=110728828;

RN RX MEDLINE=20191172; PubMed=110728828;

RN RA Zeng X.C., Li W.X., Zhu S.Y., Peng F., Jiang J.H., Yang F.H., Wu K., Li;

RN RT "Cloning and characterization of the cDNA sequences of two venom-

RN RS peptides from Chinese scorpion Buthus martensii Karsch (BmK);"

RN Toxicon 38:893-899;(2001).

RN [2] -

RN SEQUENCE FROM N.A.

RN STRAIN=10; TISSUE=Venom gland;

RN RC Zeng X.C., Li W.X., Zhu S.Y.,

RN RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

RN CC -!- SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY).

RN CC -!- SIMILARITY: BELONGS TO THE A_nPHA/BETA-SCORPION TOXIN FAMILY.

RN EVBL: AF310023; AACK38091;

DR InterPro: IPR003611; Knot1.

DR InterPro: IPR0031219; Neurotoxin.

DR InterPro: IPR002061; Scorpion_toxin.

DR PFC0517; Toxin-3; 1.

DR PRINTS: PH000284; TOXIN.

DR PRODOM: PH000398; Scorpion_toxin.

DR SMART: SM05035; Knot1; 1.

DR SMART: SM05035; Knot1; 1.

KW Ionic channel.

SQ SEQUENCE 85 AA: 9412 MW: 2FFC463E025EFS7E1 CRC64;

Alignment Scores:

Pred. No. :

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

Length:

Matches:

Conservative:

Mismatches:

Indels:

Gaps:

QY 52 TGCACAGGTGAGTGCAAGAGGGGTTAAAGGGTGGTCACTGC-----3GTRRC 102

DB 41 CysAspAspGlyCysLysAsnGlyA:agluserGlyTyrcysGinTrpA:aglyva: fc

QY 103 TTCGCTAACGTGAAACTGCTGGTGC 126

DB 61 TyrGlyAsnAla--CysTrpCys 67

Search completed: October 16, 2003, 17:16:13

Job time : 40.0293 secs

Alignment Scores:

Pred. No. :

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

Length: 136

Matches: 16

Conservative: 3

Mismatches: 17

Indels: 7

Gaps: 3

US-09-673-274B-2_COPY_1_132 (1-132) x Q9VZR3 (1-106)

4 AACGTTATCGTTCTGCG---GTTGGGGTCTGCAACTACKCTCCGATGCCGT 60

68 LystyrylLyProCysAlaValAtrpAsp-----AsnGluMetCysArgArg 83

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen, ltd.

DNM nucleic - protein search, using frame_plus_n2p model

Run on: October 16, 2003, 17:12:07 : Search time 27.4086 Seconds

(without alignments)
15.8-850 Million cell updates/sec

Title: US-09-673-274B-2_COPY_1_132

Perfect score: 267

Sequence: 1 gataaqtatcgdttcgtq.....tgaaactgtgtgtcgagact .32

Scoring table: BLOSUM62

Xgapext 10.0 , Xgapext 0.5

Ygapop 10.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Deltop 6.0 , Delext 7.0

Searched: 609560 seqs, 1639171C2 residues

Total number of hits satisfying chosen parameters: 1219120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

```
MODEL:frame+ n2p model -DEV=xlp
-i-/cgn2.1-USPTO spool/US0967324/runat 16102003170630 2743/app_query.fasta_1 654
-DB=Published App1
SEQUENCES_AA -QFORMAT=gzSTAN
-LOOPCL=0 -LOOPEXT=0
UNITS=bits START=1 -END=1 -MATRIX=b1esum62
TRANS=human40.cgi -LIST=45 -DOALIGN=C -SCORE=PCT -THR MAX=100
THR MIN=0 -ALIGN=P -MODE=LOCAL -OUTfmt=sto -NORMALIZ=1 -HEAPSIZE=500 -MINLEN=0
MAXLEN=20000000000 -USER=US09673274 @CGN 1 1.10@US03003 170630 2743
NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT =0 -DSBLOCK=100
LONGLOC -DEV TIMEOUT=120 -WARN TIMEOUT=30 -TREACCS=1 -XGAPOP=10 -XGAPEXT=0.5
FGAPOP=6 -FGAPEXT=7 -YGAPEXT=c .5 -DELEX=6 -DEL0P=6
Database : Published_Applications_AA.*
```

/cgn2_6/podata/2/pubpa/US09_PUBCOMB.pep:*

/cgn2_6/podata/2/pubpa/BCT_News_PUB.pep:*

/cgn2_6/podata/2/pubpa/US06_NEWS_PUB.pep:*

/cgn2_6/podata/2/pubpa/US07_FUBCOMB.pep:*

/cgn2_6/podata/2/pubpa/US07_NEW_PUB.pep:*

/cgn2_6/podata/2/pubpa/US08_FUBCOMB.pep:*

/cgn2_6/podata/2/pubpa/US08_NEWS_PUB.pep:*

/cgn2_6/podata/2/pubpa/US09A_PUBCOMB.pep:*

/cgn2_6/podata/2/pubpa/US09B_PUBCOMB.pep:*

/cgn2_6/podata/2/pubpa/US09C_PUBCOMB.pep:*

/cgn2_6/podata/2/pubpa/US09_NEW_PUB.pep:*

/cgn2_6/podata/2/pubpa/US10A_PUBCOMB.pep:*

/cgn2_6/podata/2/pubpa/US10B_PUBCOMB.pep:*

/cgn2_6/podata/2/pubpa/US10C_PUBCOMB.pep:*

/cgn2_6/podata/2/pubpa/US10_NEW_PUB.pep:*

/cgn2_6/podata/2/pubpa/US60_NEW_PUB.pep:*

/cgn2_6/podata/2/pubpa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query | Match Length | DB ID | Description |
|------------|-------|-------|--------------|-------------------|-------------------|
| 1 | 232 | 86.9 | 15 | US-13-125-258-1:9 | Sequence 113, APP |

| | | | | | |
|----|------|------|-----|----------------------|--------------------|
| 2 | 232 | 86.9 | 73 | US-15-125-258-1:17 | Sequence 117, APP |
| 3 | 79.5 | 29.8 | 65 | US-0-264-48C-1:3 | Sequence 13, APP |
| 4 | 79.5 | 29.8 | 66 | US-10-264-48C-1:4 | Sequence 11, APP |
| 5 | 76.5 | 28.7 | 61 | US-10-264-48C-9 | Sequence 9, APP |
| 6 | 75 | 28.1 | 61 | US-09-929-481-2 | Sequence 2, APP |
| 7 | 74.5 | 27.9 | 44 | US-10-180-247-4 | Sequence 4, APP |
| 8 | 74.5 | 27.9 | 69 | US-10-180-247-6 | Sequence 6, APP |
| 9 | 74.5 | 27.9 | 70 | US-10-180-247-2 | Sequence 2, APP |
| 10 | 71.5 | 26.8 | 61 | US-10-264-480-6 | Sequence 6, APP |
| 11 | 71.5 | 26.8 | 61 | US-10-264-480-7 | Sequence 7, APP |
| 12 | 71.5 | 26.8 | 61 | US-10-264-480-8 | Sequence 8, APP |
| 13 | 71 | 26.6 | 47 | US-10-178-213-41:1 | Sequence 41, APP |
| 14 | 71 | 26.6 | 77 | US-10-178-213-10:1 | Sequence 410, APP |
| 15 | 70.5 | 26.4 | 47 | US-10-178-213-387 | Sequence 387, APP |
| 16 | 70.5 | 26.4 | 65 | US-10-264-480-14 | Sequence 14, APP |
| 17 | 70.5 | 26.4 | 84 | US-10-178-213-386 | Sequence 386, APP |
| 18 | 70.5 | 26.4 | 87 | US-10-264-480-15 | Sequence 10, APP |
| 19 | 69.5 | 26.0 | 84 | US-10-264-480-18 | Sequence 18, APP |
| 20 | 69 | 25.8 | 47 | US-10-178-213-408 | Sequence 408, APP |
| 21 | 69 | 25.8 | 47 | US-10-178-213-444 | Sequence 444, APP |
| 22 | 69 | 25.8 | 77 | US-10-178-213-407 | Sequence 407, APP |
| 23 | 69 | 25.8 | 78 | US-10-178-213-443 | Sequence 443, APP |
| C | 68.5 | 26.1 | 173 | US-10-156-761-7787 | Sequence 7787, APP |
| 24 | 68.5 | 26.1 | 86 | US-10-178-213-396 | Sequence 396, APP |
| 25 | 68 | 25.5 | 47 | US-10-178-213-395 | Sequence 395, APP |
| 26 | 68 | 25.5 | 76 | US-10-178-213-395 | Sequence 395, APP |
| 27 | 67.5 | 26.3 | 81 | US-10-264-480-12 | Sequence 12, APP |
| 28 | 67 | 25.4 | 45 | US-10-178-213-168 | Sequence 168, APP |
| 29 | 67 | 25.1 | 72 | US-10-178-213-167 | Sequence 167, APP |
| 30 | 67 | 25.1 | 86 | US-10-178-213-480-22 | Sequence 22, APP |
| 31 | 67 | 25.1 | 86 | US-10-178-213-480-23 | Sequence 23, APP |
| 32 | 66.5 | 24.9 | 47 | US-10-178-213-3C9 | Sequence 309, APP |
| 33 | 66.5 | 24.9 | 47 | US-10-178-213-339 | Sequence 339, APP |
| 34 | 66.5 | 24.9 | 58 | US-10-264-480-4 | Sequence 4, APP |
| 35 | 66.5 | 24.9 | 62 | US-10-244-359-21 | Sequence 21, APP |
| 36 | 66.5 | 24.9 | 66 | US-10-264-480-15 | Sequence 15, APP |
| 37 | 66.5 | 24.9 | 71 | US-10-178-213-308 | Sequence 308, APP |
| 38 | 66.5 | 24.9 | 84 | US-10-178-213-338 | Sequence 338, APP |
| 39 | 65.5 | 24.5 | 44 | US-10-178-213-147 | Sequence 147, APP |
| 40 | 65.5 | 24.5 | 58 | US-10-264-480-3 | Sequence 3, APP |
| 41 | 65.5 | 24.5 | 71 | US-10-178-213-146 | Sequence 146, APP |
| 42 | 65 | 24.3 | 45 | US-10-178-213-210 | Sequence 210, APP |
| 43 | 65 | 24.3 | 47 | US-10-178-213-447 | Sequence 3, APP |
| 44 | 65 | 24.3 | 47 | US-10-178-213-447 | Sequence 447, APP |
| 45 | 65 | 24.3 | 47 | US-10-178-213-450 | Sequence 450, APP |

ALIGNMENTS

RESULT 1

US-10-125-258-1:19

Sequence 119, Application US-10-125-258

Publication No. US2010028320A1

GENERAL INFORMATION

Applicant: Altier, Daniel J.

Applicant: Hermann, Rafea;

Applicant: Li, Albert L.

Applicant: McCutchen, Billy F.

Applicant: Presnail, James K.

Applicant: Weaver, Janine L.

Applicant: Wong, James F. H.

TITLE OF INVENTION: Antimicrobial Peptides and Their

Title of Invention: Uses

File Reference: 35718/246215

Current Application Number: US-10-125-258

Current Filing Date: 20CC2-04-18

Prior Application Number: 60/285,355

Prior Filing Date: 2001-04-22

Number of SEQ ID NOS: 127

Software: FastSEQ for Windows Version 4.0

Seq ID No: 119

Length: 44

Type: PRT

ORGANISM: Agrotis ipsilon
S-12-125-258-119

RESULT 3
US-10-264-480-13

; Sequence 13, Application US/10264480
; Publication No. US20030113892A1
; GENERAL INFORMATION:
; APPLICANT: Hammock, Bruce D.
; INVENTION: ISOLATED POLYPEPTIDES AND COMPOSITIONS
; FROM THE VENOM OF P. TRANSVAALICUS AND METHODS OF USE
; FILE REFERENCE: JCAL256
; CURRENT APPLICATION NUMBER: US/10/264,480
; CURRENT FILING DATE: 2002-10-04
; PRIORITY NUMBER: 60/393,070
; PRIORITY FILING DATE: 2002-06-28
; PRIORITY APPLICATION NUMBER: 60/327,602
; PRIORITY FILING DATE: 2001-03-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version: 4.0
; SEQ ID NO: 13
; LENGTH: 65
; TYPE: PRT
; ORGANISM: Centruroides sculpturatus
US-10-264-480-13

SEQUENCE 13
Length: 44
Matches: 38
Conservative: 2
Mismatches: 3
Indels: 0
Gaps: 0

Alignment Scores:
Percent Similarity: 93.02%
Best Local Similarity: 88.37%
Query Match: 86.89%
B.: 15

US 69 673 274B 2_COPY_1_132 (:132) x US-10-125 256-1:9 (1-44)
y : GATAAGCTTATCGGTCTCGGTGGTGTAACTACACTCCATTGCCAACGGT 6C
y : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
y : AspValAlaIleGlySerCysVal:ArgGlyAsp:Asp:AsnCysAsnAsn 2C
y : 61 GAGTGCAGAGGAGGGCTTACAGGTGGTCACTCGGTCTCGCTAACGTGAACTC 12C
y : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
y : 2: GlucCysLysA:ArgGlyTyrryrsCysGly:HisCysGlySerPheAlaAsnValAsnCys 4C
b : 121 TGGTGCAG 129
y : |||||:|||||:
b : 41 TrpCysGlu 43

SEQUENCE 14
Length: 65
Matches: 55
Conservative: 17
Mismatches: 3
Indels: 12
Gaps: 3

Alignment Scores:
Percent Similarity: 51.28%
Best Local Similarity: 43.59%
Query Match: 29.78%
DE: 15
B.: 3

US-09-673-274B-2_COPY_1_132 (1-132) x US-10-264-480-13 (1-65)

Qy : 19 TGGTGTGGGTGGTGTGAACTACCTCCGATGCCAACGGTGAAGGAGGGGT 65
Qy : |||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db : 16 CysPheTrpLeuGlySerAla:AsnThrGlyCysLysAla:Asn 33
Db : 79 TACAGGCT:----GSTACTGGTCTCTCCCTAACGTGAACCTGTTGGAG 129
Db : 34 GluGlyGlySer:Gly:GlyCys:TyrryrsCys:AsnAla:-----:CysTrpCysGlu 49

RESULT 4
US-10-264-480-12

; Sequence 12, Application US/10264480
; Publication No. US20030113892A1
; GENERAL INFORMATION:
; APPLICANT: Hammock, Bruce D.
; INVENTION: ISOLATED POLYPEPTIDES AND COMPOSITIONS
; FROM THE VENOM OF P. TRANSVAALICUS AND METHODS OF USE
; FILE REFERENCE: UCAL256
; CURRENT APPLICATION NUMBER: US/10/264,480
; CURRENT FILING DATE: 2002-10-04
; PRIORITY NUMBER: 60/393,070
; PRIORITY FILING DATE: 2002-06-28
; PRIORITY APPLICATION NUMBER: 60/327,602
; PRIORITY FILING DATE: 2001-03-04
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version: 4.0
; SEQ ID NO: 12
; LENGTH: 73
; TYPE: PRT
; ORGANISM: Agrotis ipsilon
US-10-125-258-17

SEQUENCE 12
Length: 73
Matches: 39
Conservative: 2
Mismatches: 3
Indels: 0
Gaps: 0

Alignment Scores:
Percent Similarity: 93.02%
Best Local Similarity: 88.37%
Query Match: 86.89%
B.: 15

US-09-673-274B 2_COPY_1_132 (1-132) x US-10-125-258-1:7 (1-73)
y : GATAAGGTTATCGGTCTCGGTGCTGACTCACCTCGGTCACTCCGTTGCCAACGGT: 6C
y : |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
y : AspValAlaIleGlySerCysVal:ArgGlyAsp:Asp:AsnCysAsnAsn 49
y : 61 GAGTGCAGAGGAGGGCTTACAGGTGGTCACTCGGTCTCTCCGTTAACGTGAACTC 12C
y : |||||:|||||:|||||:|||||:|||||:|||||:
y : 50 GlucCysLysA:ArgGlyTyrryrsCysGly:HisCysGlySerPheAlaAsnValAsnCys 69
b : 221 TGGTGCAG 129
y : |||||:
b : 70 TrpCysGlu 72

SEQUENCE 15
Length: 66
Matches: 56
Conservative: 17
Mismatches: 4
Indels: 7

Alignment Scores:
Percent Similarity: 53.85%
Best Local Similarity: 43.59%
Query Match: 29.78%

GENERAL INFORMATION:
 APPLICANT: DeRose, Richard
 APPLICANT: Freysinet, Georges
 ATTORNEY: Hoffman, Jules
 TITLE OF INVENTION: Vector Containing Drosomycin, It and Production of Disease-Resistant
 TITLE OF INVENTION: Transgenic Plants
 FILE REFERENCE: A32889-PCT-USA-A-072667-0:52
 CURRENT APPLICATION NUMBER: US/11C/180, 247
 CURRENT FILING DATE: 2000-06-26
 PRIOR APPLICATION NUMBER: PCT/FR99/0:462
 PRIOR FILING DATE: 2000-01-21
 PRIOR APPLICATION NUMBER: PCT/FR97/09, 1:5
 PRIOR FILING DATE: 1997-07-08
 PRIOR APPLICATION NUMBER: FR97/09, 1:5
 PRIOR FILING DATE: 1997-07-11
 PRIOR APPLICATION NUMBER: FR97/09, 663
 PRIOR FILING DATE: 1997-07-24
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 6
 LENGTH: 69
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Ubiquitin-drosomycin fusion peptide

Length: 69
 Matches: 15
 Conservative: 2
 Best Local Similarity: 37.50%
 Query Match: 27.90%
 DB: 12
 Gaps: 3

US-09-673-274B-2_COPY_1_132 (1-132) × US-10-180-247-2 (1-70)

Qy 13 GGTTCTGC--GTGGGGTGTGAACTACACTCCGATTCGAGTGCACCGTGACTGCAAG 69
 Db 35 GlyPrCsA-avaIrpAsP-----AsnGluThrCysArgArgValCysSys 50
 Qy 70 AGAGGGTTACAAGGGTGTACTGGTTCTCGTAACGTGAACTGGTGTGCAG 129
 Db 51 GluGluGlyArgSerSerGlyHisCysSer----ProSerLeuLysCystPcysGlu 68

RESULT 10
 US-10-264-480-6
 Sequence 6, Application US/10264480
 Publication No. US20030113892A1
 GENERAL INFORMATION:
 APPLICANT: Hammock, Bruce D.
 ATTORNEY: Ineoglu, Bora
 TITLE OF INVENTION: ISOLATED POLYPEPTIDES AND COMPOSITIONS FROM THE VENOM OF P. TRANSVAALICUS AND METHODS OF USE
 FILE REFERENCE: UCAL256
 CURRENT APPLICATION NUMBER: US/10/264, 480
 CURRENT FILING DATE: 2002-10-04
 PRIOR APPLICATION NUMBER: 60/393,070
 PRIOR FILING DATE: 2002-06-28
 PRIOR APPLICATION NUMBER: 60/327,602
 PRIOR FILING DATE: 2001-10-04
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 6
 LENGTH: 61
 TYPE: PRT
 ORGANISM: Butthacus arenicola
 US-10-264-480-6

Alignment Scores:
 Pred. No.: 0.387
 Score: 74.50
 Percent Similarity: 42.50%
 Best Local Similarity: 37.50%
 Query Match: 27.90%
 DB: 12
 Gaps: 3

US-09-673-274B-2_COPY_1_132 (1-132) × US-10-180-247-6 (1-69)

Qy 13 GGTTCTGC--GTGGGGTGTGAACTACACTCCGATTCGAGTGCACCGTGACTGCAAG 69
 Db 34 GlyPrCsA-avaIrpAsP-----AsnGluThrCysArgArgValCysSys 49
 Qy 70 AGAGGGTTACAAGGGTGTACTGGTTCTCGTAACGTGAACTGGTGTGCAG 129
 Db 50 GluGluGlyArgSerSerGlyHisCysSer----ProSerLeuLysCystPcysGlu 67

RESULT 9
 US-10-180-247-2
 Sequence 2, Application US/10182247
 Publication No. US20030167519A1
 GENERAL INFORMATION:
 APPLICANT: DeRose, Richard
 ATTORNEY: Freysinet, Georges
 ATTORNEY: Hoffman, Jules
 TITLE OF INVENTION: Vector Containing Drosomycin, It and Production of Disease-Resistant
 TITLE OF INVENTION: Transgenic Plants
 FILE REFERENCE: A32889-PCT-USA-A-072667-0:182
 CURRENT APPLICATION NUMBER: US/11C/180, 247
 CURRENT FILING DATE: 2000-06-26
 PRIOR APPLICATION NUMBER: 09/488, 251
 PRIOR FILING DATE: 2000-01-11
 PRIOR APPLICATION NUMBER: PCT/FR98/01462
 PRIOR FILING DATE: 1998-07-08
 PRIOR APPLICATION NUMBER: FR97/09, 115
 PRIOR FILING DATE: 1997-07-11
 PRIOR APPLICATION NUMBER: FR97/09, 663
 NUMBER OF SEQ ID NOS: 15
 SEQ ID NO: 2
 LENGTH: 70
 TYPE: PRT

Alignment Scores:
 Pred. No.: 0.388
 Score: 74.50
 Percent Similarity: 42.50%
 Best Local Similarity: 37.50%
 Query Match: 27.90%
 DB: 12
 Gaps: 3

US-09-673-274B-2_COPY_1_132 (1-132) × US-10-264-480-6 (1-61)

Qy 16 TCTGGGTGTGGGTGTGAACTACACTCCGATTCGAGTGCACCGTGACTGCAAGGGGG 75
 Db 13 SerCysLeuPheGly-----AsnGluGlyCysAspLysGluClysAlaTyr 28

Qy 76 GGTTACAGGGTGTCACTGGGTTCCTCGTAACGTGAACTGGTGTGCAG 129
 Db 29 GlyGlySerGlyArgSerGlyCystPcysGlu 45

RESULT 11
 US-10-264-480-7
 Sequence 7, Application US/10264480
 Publication No. US20030113892A1
 GENERAL INFORMATION:
 APPLICANT: Hammock, Bruce D.
 ATTORNEY: Ineoglu, Bora
 TITLE OF INVENTION: ISOLATED POLYPEPTIDES AND COMPOSITIONS FROM THE VENOM OF P. TRANSVAALICUS AND METHODS OF USE
 FILE REFERENCE: UCAL256

CURRENT APPLICATION NUMBER: US/10/264,480
 CURRENT FILING DATE: 2002-10-04
 PRIOR APPLICATION NUMBER: 60/393,070
 PRIOR FILING DATE: 2002-06-28
 PRIOR APPLICATION NUMBER: 60/327,602
 PRIOR FILING DATE: 2001-10-04
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 8
 LENGTH: 61
 TYPE: PRT
 ORGANISM: *Buthus occitanus*
 S-10-264-480-7

Alignment Scores:
 Pred. No.: 0.932 Length: 61
 core: 71.50 Matches: 14
 percent Similarity: 55.26% Conservative: 7
 best Local Similarity: 36.84% Mismatches: 12
 Query Match: 26.78% Indels: 5
 DB: 15 Gaps: 2

US-09-673-274B-2_COPY_1_132 (1-132) × US-10-264-480-7 (1-61);
 Qy 16 TCCGGCTGTGGGGTGTGAACTACACTTCGATGCCAACGGTGAAGGAGG 75
 Db 13 SerCysLeuPheGly-----AsnGluGlyCysAspLysAlaTyr 28

Qy 76 GGTACAGGGTGTCACTGGGTCTCTCGCTAAGCTGAAGTGTGG 129
 Db 29 GlyGlySerTyrGlyTyrCysTrpThrTrp--GlyLeuAlaCysTrpCysGlu 45

RESULT 12 US-10-264-480-8

Title of Invention: ISOLATED POLYPEPTIDES AND COMPOSITIONS

Title of Invention: FROM THE VENOM OF P. TRANSVAALICUS AND METHODS OF USE

FILE REFERENCE: UCAL256

CURRENT APPLICATION NUMBER: US/10/264,480

CURRENT FILING DATE: 2002-10-04

PRIOR APPLICATION NUMBER: 60/393,070

PRIOR FILING DATE: 2002-06-28

PRIOR APPLICATION NUMBER: 60/327,602

PRIOR FILING DATE: 2001-10-04

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 8

LENGTH: 61

TYPE: PRT

ORGANISM: *Buthus occitanus*

S-10-264-480-8

Alignment Scores:

Pred. No.: 0.932 Length: 61
 core: 71.50 Matches: 14
 percent Similarity: 55.26% Conservative: 7
 best Local Similarity: 36.84% Mismatches: 12
 Query Match: 26.78% Indels: 5
 DB: 15 Gaps: 2

RESULT 13 US-09-673-274B-2_COPY_1_132 (1-132) × US-10-264-480-8 (1-61);

Qy 16 TCCGGCTGTGGGGTGTGAACTACACTTCGATGCCAACGGTGAAGGAGG 75
 Db 13 SerCysLeuPheGly-----AsnGluGlyCysAspLysAlaTyr 28

Qy 76 GGTACAGGGTGTCACTGGGTCTCTCGCTAAGCTGAAGTGTGG 129
 Db 29 GlyGlySerTyrGlyTyrCysTrpThrTrp--GlyLeuAlaCysTrpCysGlu 45

RESULT 13 US-10-213-411

Sequence 410, Application US/10/178213
 Publication No. US2003041348A1
 GENERAL INFORMATION:
 APPLICANT: Simmons, Carl R.
 APPLICANT: Navarro Acevedo, Pedro A.
 APPLICANT: Harvell, Leslie
 APPLICANT: Catton, Rebecca
 APPLICANT: McCutchen, Billy Fred
 APPLICANT: Lu, Albert
 APPLICANT: Herrmann, Rafael
 APPLICANT: Wong, James
 TITLE OF INVENTION: Defensin Polypeptides and Methods of Use
 FILE REFERENCE: 35718/246703
 CURRENT APPLICATION NUMBER: US/10/178213
 PRIOR APPLICATION NUMBER: 60/300,152
 PRIOR FILING DATE: 2001-06-22
 PRIOR APPLICATION NUMBER: 60/300,241
 NUMBER OF SEQ ID NOS: 469
 SOFTWARE: FastSEQ for Windows Version 4.0

US-09-673-274B-2_COPY_1_132 (1-132) × US-10-213-411 (1-47)

Qy 13 GGTCCCTGCGTGTGGGTCTGTGAAGTACACTTCGATGCCAACGGTGAAGGAGG 72
 Db 12 GlyProCys1-----SerGlyThrAsnCysAlaSerValCysLysTrp: 26
 Query Match: 36.84%
 DB: 26.59%
 Gaps: 15

US-09-673-274B-2_COPY_1_132 (1-132) × US-10-178-213-411 (1-47)

Qy 13 GGTCCCTGCGTGTGGGTCTGTGAAGTACACTTCGATGCCAACGGTGAAGGAGG 72
 Db 12 GlyProCys1-----SerGlyThrAsnCysAlaSerValCysLysTrp: 26
 Query Match: 36.84%
 DB: 26.59%
 Gaps: 15

RESULT 14 US-10-178-213-410

Sequence 410, Application US/10/178213
 Publication No. US2003041348A1
 GENERAL INFORMATION:
 APPLICANT: Simmons, Carl R.
 APPLICANT: Navarro Acevedo, Pedro A.
 APPLICANT: Harvell, Leslie
 APPLICANT: Catton, Rebecca
 APPLICANT: McCutchen, Billy Fred
 APPLICANT: Lu, Albert
 APPLICANT: Herrmann, Rafael
 APPLICANT: Wong, James
 TITLE OF INVENTION: Defensin Polypeptides and Methods of Use
 FILE REFERENCE: 35718/246703
 CURRENT APPLICATION NUMBER: US/10/178,213
 PRIOR APPLICATION NUMBER: 60/300,152
 PRIOR FILING DATE: 2001-06-22
 PRIOR APPLICATION NUMBER: 60/300,241
 NUMBER OF SEQ ID NOS: 469
 SOFTWARE: FastSEQ for Windows Version 4.0

SEQ. ID NO. 410
LENGTH: 77
TYPE: PRT
ORGANISM: *tropaneum majus*
S-13-178-213 410

Search completed: October 16, 2003, 17:34:08
Job time : 28.4c86 secs

GenCore version 5.1.6
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M nucleic - protein search, using frame_plus_n2p mode:

un on: October 16, 2003, 17:06:37 ; Search time 13:561 Seconds
 (without alignments)
 849.038 Million cell updates/sec

title: US-09-673-274B-2_COPY_1_132

erfect score: 1 gataagcttacgtttccgtgact 132

coring table: BL050M62

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 Ygapext 10.0 , Ygapext 0.5
 Fgapext 6.0 , Fgapext 7.0
 Delop 6.0 , Delext 7.0

searched: 328717 seqs, 4210858 residues

otal number of hits satisfying chosen parameters: 657414

minimum DB seq length: 0
 maximum DB seq length: 2000000000

ost-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Command line parameters:
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 DB=1 Issued Patents AA -QFMT=fastan -SUFFIX=x-rai -MINMATCH=0.1 -LOPCL=0
 LOOPEXT=0 -UNITS=bits START=1 -END=1 -MATRIX=b10sum62 -TRANS=human0.cdi
 LIST=45 -DOALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
 MODE=LOCAL -OUTFILE=ext -NORM=ext -HEAPSIZE=500 -MINLEN=0
 NO MMNP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
 DEV TIMEOUT=120 -WARN TIMEOUT=10 -THREADS=1 -XGAPOP=1C -XGAPEXT=0.5 -FGAPOP=6
 FGAPEXT=7 -YGAPOD=10 -YGAPEXT=0.5 -DELEXI=7

atabase : Issued Patents AA:*

1: /cgn2.6/ptodata/1/iaa/5A_COMBO.pep:*

2: /cgn2.6/ptodata/1/iaa/5B_COMBO.pep:*

3: /cgn2.6/ptodata/1/iaa/6A_COMBO.pep:*

4: /cgn2.6/ptodata/1/iaa/6B_COMBO.pep:*

5: /cgn2.6/ptodata/1/iaa/PCTUS_COMBO.pep:*

6: /cgn2.6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Query Score | Match Length | DB ID | Description |
|------------|-------------|--------------|------------------------------|--------------------|
| 1 | 80.5 | 30.1 | 65 1 US-09-435-040-2 | Sequence 2, Appli |
| 2 | 76.5 | 28.7 | 65 3 US-09-020-216-2 | Sequence 2, Appli |
| 3 | 76.5 | 28.7 | 61 1 US-08-682-485A-25 | Sequence 4, Appli |
| 4 | 76.5 | 28.7 | 61 1 US-08-451-472-4 | Sequence 4, Appli |
| 5 | 76.5 | 28.7 | 61 2 US-08-933-314-25 | Sequence 5, Appli |
| 6 | 74.5 | 27.9 | 44 4 US-08-480-251-4 | Sequence 6, Appli |
| 7 | 74.5 | 27.9 | 69 4 US-09-480-251-6 | Sequence 6, Appli |
| 8 | 74.5 | 27.9 | 70 4 US-09-480-251-2 | Sequence 2, Appli |
| 9 | 74 | 27.7 | 64 4 US-09-403-343B-25 | Sequence 2, Appli |
| c 10 | 68 | 28.9 | 147 4 US-09-252-991A-16810 | Sequence 16810, A |
| c 11 | 68 | 28.9 | 149 4 US-09-252-991A-32270 | Sequence 32270, A |
| 67 | 67 | 25.1 | 63 4 US-09-252-991A-20063 | Sequence 6, Appli |
| 14 | 64.5 | 24.2 | 80 3 US-09-220-216-3 | Sequence 3, Appli |
| 15 | 64.5 | 24.2 | 80 3 US-08-952-383A-14 | Sequence 4, Appli |
| 16 | 64.5 | 24.2 | 26 4 US-08-264A-27 | Sequence 27, Appli |
| 17 | 63.5 | 23.8 | 61 1 US-08-682-485A-26 | Sequence 26, Appli |
| 18 | 63.5 | 23.8 | 61 2 US-08-933-314-26 | Sequence 26, Appli |
| c 19 | 63 | 26.8 | 314 2 US-08-460-309-19 | Sequence 19, Appli |
| c 20 | 62 | 23.2 | 314 2 US-08-125-077-19 | Sequence 19, Appli |
| 21 | 62 | 23.2 | 74 4 US-09-442-631-4 | Sequence 4, Appli |
| 22 | 61.5 | 23.0 | 75 1 US-08-289-458-2 | Sequence 2, Appli |
| 23 | 61.5 | 23.0 | 75 2 US-08-761-559-2 | Sequence 2, Appli |
| 24 | 61.5 | 23.0 | 75 3 US-09-127-646-2 | Sequence 2, Appli |
| 25 | 61.5 | 23.0 | 288 4 US-09-252-991A-31433 | Sequence 31433, A |
| c 26 | 61.5 | 26.2 | 361 3 US-09-231-227-4 | Sequence 4, Appli |
| c 27 | 61.5 | 26.2 | 361 4 US-09-768-585-4 | Sequence 4, Appli |
| c 28 | 61 | 26.2 | 336 4 US-09-252-991A-32162 | Sequence 32162, A |
| c 29 | 61 | 26.2 | 68 3 US-09-053-022-1 | Sequence 1, Appli |
| c 30 | 60.5 | 22.7 | 68 3 US-09-053-022-4 | Sequence 9, Appli |
| c 31 | 60.5 | 22.7 | 91 3 US-09-053-022-9 | Sequence 9, Appli |
| c 32 | 58.5 | 22.1 | 159 4 US-09-599-266A-11 | Sequence 1, Appli |
| c 33 | 58.5 | 21.9 | 67 3 US-09-353-021-2 | Sequence 2, Appli |
| c 34 | 58 | 21.7 | 54 1 US-08-656-318A-1 | Sequence 1, Appli |
| c 35 | 58 | 21.7 | 54 2 US-08-956-459-1 | Sequence 5, Appli |
| c 36 | 58 | 21.7 | 62 1 US-08-451-472-5 | Sequence 2234, A |
| c 37 | 58 | 21.7 | 62 1 US-09-09-252-991A-22787 | Sequence 2234, A |
| c 38 | 57.5 | 24.5 | 518 4 US-09-252-991A-25967 | Sequence 25967, A |
| c 39 | 57.5 | 24.5 | 518 4 US-08-185-432-17 | Sequence 17, Appli |
| c 40 | 57.5 | 21.5 | 2556 1 US-08-383-590A-20 | Sequence 20, Appli |
| c 41 | 57.5 | 21.5 | 2556 3 US-08-532-384-20 | Sequence 20, Appli |
| c 42 | 57.5 | 21.5 | 2556 4 US-08-899-232-2 | Sequence 2234, A |
| c 43 | 57 | 24.3 | 245 4 US-09-252-991A-22334 | Sequence 2234, A |
| c 44 | 57 | 24.3 | 526 4 US-09-252-991A-23462 | Sequence 23462, A |

ALIGNMENTS

RESULT 1

US-09-435-040-2

; Sequence 1, Application US-09415040

; CORRESPONDENCE ADDRESS:

; Patent No. 5756310

; GENERAL INFORMATION:

; APPLICANT: Hammock, Bruce D.

; APPLICANT: Herrmann, Rafael

; APPLICANT: Moskowitz, Haim

; TITLE OF INVENTION: Insect Control With Multiple Toxins

; NUMBER OF SEQUENCES: 3

; SEQUENCE 1, Application US-09415040

; Sequence 2, Application US-09415040

; Sequence 3, Application US-09415040

COUNTRY: U.S.A.

21P: 94111-4121

COMPUTER READABLE FORM: COMPUTER TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS-MS-DOS

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US-08/435,040

FILING DATE: 08-MAY-1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Siebert, J. Suzanne

REGISTRATION NUMBER: 28,758

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 362-5556

TELEFAX: (415) 362-5418

TELEX: 278338 MGPS

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 65 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 US-09-020-216-2

Alignment Scores:
 Pred. No.: 0.0127 Length: 65 Score: 80.50
 Score: 80.50 Matches: 80.50
 Percent Similarity: 57.14% Percent Similarity: 57.14%
 Best Local Similarity: 40.48% Best Local Similarity: 40.48%
 Query Match: 30.15% Query Match: 30.15%
 DB: 9 MisMatches: 5
 DB: 9 Indels: 3
 DB: 9 Gaps: 4

JS-09-673-274B-2_CCPY_1_132 (1-132) × US-09-020-216-2 (1-65)

QY 16 TCCCTGCCGTGG-----GGTGCCTGTAACACTACACTTCGATTCGGTAGTGCAAG 69
 CY 16 TCCCTGCCGTGG-----GGTGCCTGTAACACTACACTTCGATTCGGTAGTGCAAG 69
 DB 12 AsnCysValTyrThrCysGlyAlaSerItyr-----CysAsnThrGlyCysThr 28
 QY 70 AGGAGGGTTAACAGGGTGGTCACTGC-----GGTTCCTTGCTAACGTGAACTGC 120
 DB 29 LysAsnGlyAlaGluSerItyrCysGlnTrpPheGlyLysTyrCysGlnTrpPheGlyAsnAla---Cys 47
 QY 121 TGTGC 126
 DB 48 TrpCys 49

RESULT 3
 US-C8-682-485A-25
 Sequence 25, Application US/06682485A
 Patent No. 5763568

GENERAL INFORMATION:
 APPLICANT: ATKINSON, RONALD K.
 APPLICANT: HOWDEN, MERLIN E.H.
 APPLICANT: TYLER, MARGARET I.
 APPLICANT: VONARY, EDWARD J.
 TITLE OF INVENTION: Insecticidial Toxins Derived From
 TITLE OF INVENTION: Funnel Web (Arax or Hadronyche Spiders)
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Zedeca, Inc.
 STREET: 1200 South 47th Street
 CITY: Richmond
 STATE: California
 COUNTRY: USA
 ZIP: 94804

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/682,485A
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/682,485
 FILING DATE: 17-JULY-1996
 APPLICATION NUMBER: US/08/256,933
 FILING DATE: 27-JULY-1994
 APPLICATION NUMBER: WO 93/15108
 FILING DATE: 29-JAN-1993
 APPLICATION NUMBER: AU P/0722
 FILING DATE: 31-JAN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Shaw, Melissa A.
 REGISTRATION NUMBER: 38,301
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 362-5556
 TELEX: 278638 MGGS
 INFORMATION FOR SEQ ID NO: 2:
 LENGTH: 65 amino acids
 TYPE: amino acid
 TOPOLOGY: linear

SEQUENCE CHARACTERISTICS:
 LENGTH: 61 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO

ORIGINAL SOURCE:
 ORGANISM: *Leiurus quinquestriatus*
 US-08-682-485A-25

Alignment Scores:
 Aligned. No.: 0.0418
 Score: 6.50
 Percent Similarity: 55.26%
 Best Local Similarity: 39.47%
 Query Match: 28.65%
 Gaps: 5

US-09-673-274B-2_COPY_1_132 (1-132) × US-08-682-485A-25 (1-61)
 Qy 16 TCTGCTGTGGGGTGTGAACATTCGATTGAAACCGTGACTGCAAGAGGG 75
 Db 13 SerCysLeuPheGly... --- AsnGluGlyAsnAspLysGlySerTyr 28
 Qy 76 CGTTACAGGGTGTCACTGCCTTCCTCGCTAACGTGAACTGCTGGCGAG 129
 Db 29 GlyGlySerTyrGlyTyrCystrpThrTrp---GlyLeuAlaCystrpCysGlu 45

SEQUENCE 4
 US-08-451-472-4
 Sequence 4, Application US/08451472
 Patent No. 5570192

GENERAL INFORMATION:
 APPLICANT: TITLE OF INVENTION: BIOLOGICAL CONTROL AGENTS
 NUMBER OF SEQUENCES: 73
 CORRESPONDENCE ADDRESS:
 ADDRESS: Nixon & Vanderhye PC
 STREET: 8th Floor, 1100 No. 5770192th Glebe Road
 CITY: Arlington
 STATE: Virginia
 COUNTRY: USA
 ZIP: 22201-4714

PRIOR APPLICATION DATA:
 COMPUTER READABLE FORM:
 MEDIUM: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/451,472
 FILING DATE:
 CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: US 08/117,125
 FILING DATE: 24 NOV 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Mary J Wilson
 REGISTRATION NUMBER: 32,955
 TELECOMMUNICATION INFORMATION:
 REFERENCE/DOCKET NUMBER: 1117-187
 TELEPHONE: (703) 816 4000
 TELEFAX: (703) 816 4100
 TELEX: 200797 NIXN UR
 INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
 LENGTH: 61 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide

Pred. No.: 0.0418
 Score: 76.50
 Percent Similarity: 55.26%
 Best Local Similarity: 39.47%
 Query Match: 28.65%
 DB:
 RESU: 5
 US-08-933-314-25
 Sequence 25, Application US/08933314
 Patent No. 5959182

GENERAL INFORMATION:
 APPLICANT: ATKINSON, RONALD K
 ADDRESS: 1200C Scott, 47th Street
 CITY: Richmond
 STATE: California
 COUNTRY: USA
 ZIP: 94004
 COMPUTER READABLE FORM:
 MEDIUM: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/933,314
 FILING DATE:
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/682,495
 FILING DATE: 17-JULY-1996
 APPLICATION NUMBER: US/08/256,933
 FILING DATE: 27-JULY-1994
 APPLICATION NUMBER: WO 93/15,08
 FILING DATE: 29-JAN-1993
 APPLICATION NUMBER: AU PLC722
 FILING DATE: 31-JAN-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Shaw, Melissa A.
 REGISTRATION NUMBER: 38,330
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 510-231-1112
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 61 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: *Leiurus quinquestriatus*

US-08-933-314-25

Alignment Scores:
Pred. No.: 0.0418 Length: 61
Score: 76.50 Matches: 15
Percent Similarity: 55.26% Conservative: 6
Best Local Similarity: 39.47% Mismatches: 12
Query Match: 28.65% Indexes: 5
CB: 2 Gaps: 2

US-09-673-274B-2 COPY 1_132 (1-132) × US-09-933-314-25 (1-61)

Qy 16 TCTCTGGTGGGTGCTGAACTACACTCCATTGCAAACGGTAGTGAGGAGG 75
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Dc 13 SerCysLeuPheGly-----AsnGlyCysAsnLysGlyCysSsSerYr 28
Qy 16 GTTACAAAGGTGGTCACTGGTTCTCGTAACTGAATCTGCTGGSCAG 129
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Dc 29 Gly-GlySerTyrG-Y TyrCysTrpThrT-p GlyLeuAspCysTrpCysGlu 45
Qy 16 Gly-GlySerTyrG-Y TyrCysTrpThrT-p GlyLeuAspCysTrpCysGlu 45
Dc 29 Gly-GlySerTyrG-Y TyrCysTrpThrT-p GlyLeuAspCysTrpCysGlu 45

RESULT 6

/ Sequence 4, Application US/09480251

GENERAL INFORMATION:
Patent No. 6465719
APPLICANT: DeRose, Richard
APPLICANT: Freysinet, Georges
APPLICANT: Hoffman, Jules
TITLE OF INVENTION: Chimeric Gene Encoding Drosophycin, A Vector Containing It And Production Of Disease-Resistant Transgenic Plants

FILE REFERENCE: A3289-PCT-USA-A
CURRENT FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: PCT/FR98/Ci162
PRIOR FILING DATE: 1998-07-08
PRIOR APPLICATION NUMBER: FRANCE 97/09,115
PRIOR FILING DATE: 1997-07-11
PRIOR APPLICATION NUMBER: FRANCE 97C9,663
PRIOR FILING DATE: 1997-07-24
NUMBER OF SEQ ID NOS: 15
SEQ ID NO: 4
LENGTH: 44
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-480-251-4

Alignment Scores:
Pred. No.: 0.073 Length: 44
Score: 74.50 Matches: 15
Percent Similarity: 42.50% Conservative: 2
Best Local Similarity: 37.50% Mismatches: 16
Query Match: 27.90% Indexes: 7
CB: 4 Gaps: 3

US-09-673-274B-2_COPY_1_132 (1-132) × US-09-933-314-25 (1-61)

Qy 13 CGTCTCTGC--GTGTGGTGTGAACTACACTCCATTGCAAACGGTAGTGAGGAG 69
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Dc 34 GlyProCysAlaValTyrPasp-----AsnGluIutHsArgValArgSlys 49
Qy 70 AGGAGGAGTAAAGGGTGTCACTGGTTCCTTGTAACTGTGACTGTGGCAGG 129
|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
Dc 50 GluGluGlyArgSerGlyHisCysSer-----ProSerLeuIysCysTrpCysGlu 67

RESULT 8

US-09-480-251-2

/ Sequence 2, Application US/09480251

GENERAL INFORMATION:
Patent No. 6465719
APPLICANT: DeRose, Richard
APPLICANT: Freysinet, Georges
APPLICANT: Hoffman, Jules
TITLE OF INVENTION: Chimeric Gene Encoding Drosophycin, A Vector Containing It And Production Of Disease-Resistant Transgenic Plants

FILE REFERENCE: A3289-PCT-USA-A
CURRENT FILING DATE: 2000-01-11
PRIOR APPLICATION NUMBER: PCT/FR98/01462
PRIOR FILING DATE: 1998-07-08
PRIOR APPLICATION NUMBER: FRANCE 97/09,115
PRIOR FILING DATE: 1997-07-11
PRIOR APPLICATION NUMBER: FRANCE 97C9,663
NUMBER OF SEQ ID NOS: 15
SEQ ID NO: 2
LENGTH: 70
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-480-251-2

Alignment Scores:
Pred. No.: 0.077 Length: 70
Score: 74.50 Matches: 15
Percent Similarity: 42.50% Conservative: 2
Best Local Similarity: 37.50% Mismatches: 16
Query Match: 27.90% Indexes: 7

US-09-480-251-6

/ Sequence 6, Application US/09480251

GENERAL INFORMATION:
Patent No. 6465719
APPLICANT: DeRose, Richard
APPLICANT: Freysinet, Georges
APPLICANT: Hoffman, Jules
TITLE OF INVENTION: Chimeric Gene Encoding Drosophycin,

APPLICANT: TITLE OF INVENTION: BIOLOGICAL CONTROL AGENTS
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhey PC
STREET: 8th Floor, 1100 No. 577019th Glebe Road
CITY: Arlington
COUNTRY: USA
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, vers.: #, 25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/451,472
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 38/227,125
FILING DATE: 24-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Mary C. Wilson
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 117-187
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816 4000
TELEFAX: (703) 816 4100
TELEX: 222797 NIXN CR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
TOPOLOGY: linear
MOLECULE TYPE: peptide

Alignment Scores:
 ref. No.: 0.726 Length: 60
 score: 67.30 Matches: 13
 percent Similarity: 56.76% Conservative: 8
 best Local Similarity: 35.14% Mismatches: 10
 query Match: 25.39% Indexes: 6
 B: Gaps: 2

S-09 673-2743-2_CCPY_1_132 (1-132) x US-08-451472-6 (1-60)

19 TCGCTGCGGGTGTG:GAACATCACTCCGATTCGAACTGAGGGGT 78
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 14 CysLeuLysGly - AsnGlyCysAspLysGlyCysLysAlaLysGly 28
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 79 TACAAGGGTGTGACTGGTTCTCTGGTAACCTGAA-TGTTGGTGCAGS 129
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 29 GlySerTyrGlyTyrCysTrpTrpTyr---GlyLeuAlaCysTrpCysGlu 44
 :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:
 b:

RESULT 13
 S-08-435-040-3
 Sequence 3 Application US/08435040
 Patent No. 5756340
 GENERAL INFORMATION:
 APPLICANT: Hammock, Bruce D.
 APPLICANT: Hermann, Rafael
 APPLICANT: Moskowitz, Haim
 TITLE OF INVENTION: Insect Control With Multiple Toxins
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Majestic, Parsons, Siebert & Huse
 STREET: Four Embarcadero Center, Suite 1450
 CITY: San Francisco
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 94111-4211

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-A8/435,040
 FILING DATE: 08-MAY-1995
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Siebert, Suzanne
 REGISTRATION NUMBER: 28,758
 REFERENCE DOCKET NUMBER: 2500-078USC
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 362-5556
 TELEFAX: (415) 362-5418
 TELEX: 278638 MGPS
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 67 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 US-A8/435-040-3

Alignment Scores:
 Pred. No.: 0 736 Length: 6
 SCCE: 67.00 Matches: 1
 Percent Similarity: 46.15% Conservative: 5
 Best Local Similarity: 33.33% Mismatches: 1
 Query Match: 25.09% Indels: 2
 DB: 1 Gaps: 1

US-A8/435-040-2 COPY 1 132 11-1321 X US-C8A-435-040-1

Qy 16 TCCTGCCGTGGGTTGACTAAGTCGATGCAACCGTGACTGCAAGAGGGG 75
Db 12 AsnCysValTyrHisCysPheProGlySerProGlyCysAspThrLeuCysIgylAsp 31

Qy 76 GGTACAAAGGGTGTCACTGGT-----TCCTGCCTAACGTGAACTGCTGTC 126
Db 32 GlyAlaSerSerGlyIleCysGlyPheLysGluGlyHisCysGlyPheLysLeuAlaCystrpCys 50

RESULT 14
US-09-020-216-3
Sequence 3, Application US/09020216
Patent No. 6162430

GENERAL INFORMATION:
APPLICANT: Hammock, Bruce D.
APPLICANT: Hermann, Rafael
APPLICANT: Moskowitz, Haim

TITLE OF INVENTION: Insect Control With Multiple Toxins

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:
ADDRESSEE: Majestic, Parsons, Siebert & Haue
STREET: Four Embarcadero Center, Suite 1450
CITY: San Francisco, CA
STATE: California

COUNTRY: U.S.A.
ZIP: 94111-4121

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.C, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,216
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/435,040
 FILING DATE: 08-MAY-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Siebert, J. Suzanne
 REGISTRATION NUMBER: 28,758
 REFERENCE/DOCKET NUMBER: 2500.078US0
 TELEPHONE: (415) 362-5556
 TELEFAX: (415) 362-5418
 TELEX: 278638 MGPS
 INVENTION: RECOMBINANT BACULOVIRUS INSECTICIDES
 SEQUENCE CHARACTERISTICS:
 LENGTH: 67 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: N-terminal
 JS-09-020-216-3

Alignment Scores:
 Pred. No.: 0.736 Length: 67
 Score: 67.00 Matches: 3
 Percent Similarity: 46.15% Conservative: 5
 Best Local Similarity: 33.33% Mismatches: 19
 Query Match: 25.09% Indels: 2
 DB: 3 G: 1 Gaps: 1

JS-09-673-274b-2_COPY_1_132 (1-132) x US-09-020-216-3 (1-67);
 QY 16 TCCCTGGTGTGGGGTGCTGAAACTACACTTCGATTGCAA CGTGTGACTGGAGAGGAGG 75
 DB 12 AsnGlySerValTyHisCysPheProGlySerProGlySerAspThrIeuCysGlyAsp 31
 QY 76 GGTACAAAGGTGCTCACTGGGT-----TCTTCGTTAACGTGAATGCTGGTGC 126
 DB 32 GlyLaserSerGlyHisCysGlyPhethysGluGlyHisGlyLeAlaCysTrpCys 50

RESULT 15

US-08-952-383A-14
 Sequence 14 Application US/08952383A
 Patent No. 6096104

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: RECOMBINANT BACULOVIRUS INSECTICIDES

NUMBER OF SEQUENCES: 14

COMPUTER READABLE FORM: 4

MEDIUM TYPE: DISKETTE 3.5 INCH

COMPUTER: IBM

OPERATING SYSTEM: MICROSOFT WINDOWS 3.1

SOFTWARE: MICROSOFT WORD FOR WINDOWS 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/952,383A

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: FLOYD, LINDA AXAMETHY

REGISTRATION NUMBER: 33,692

REFERENCE/DOCKET NUMBER: BA-9063-A

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 80 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-952-383A-14

Alignment Scores:

Pred. No.: 1.6 Length: 80
 Score: 64.50 Matches: 13
 Percent Similarity: 52.63% Conservative: 7

Best Local Similarity: 34.21% Mismatches: 13
 Query Match: 24.16% Indels: 5
 DB: 2 Gaps: 2

US-09-673-274b-2_COPY_1_132 (1-132) x US-08-952-383A-14 (1-80);

QY 16 TCCCTGGTGTGGGGTGCTGAAACTACACTTCGATTGCAA CGTGTGACTGGAGAGGAGG 75
 DB 32 AlaCysLysLysGly-----AsnGlyCysAspLysSalaYr 47
 QY 76 GGTACAAAGGTGGTCACTGGTTCCCTCGTAACGTGAACCTGCTGGAG 129
 DB 48 GlyGlySerTyGlySerTrpTrp---GlyLeAlaCysTrpCysGlu 64

Search completed: October 16, 2003, 17:13:06
 Job time : 14.1561 secs

command line parameters:

EV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPDP=1.0 -XGAPEXT=0.5 -FGA20P=6
 GAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELEXT=7
 PIR_76:*

DOCUMENTS

RESULT :
 A29386 neurotoxin III - scorpion (*Buthus occitanus*)
 C:Species: *Buthus occitanus* Mardochei
 C:Date: 21-May-1988 #sequence revision 21-May
 C:Accession: A29386
 R:Vargas, O.; Martin, M.F.; Rochat, H.
 Eur. J. Biochem. 162, 589-599, 1987
 A:Title: Characterization of six toxins from
 A:Reference number: A29386; MTID: 92161629; FN:
 A:Accession: A29386
 A:Molecule type: protein
 A:Residues: 1-66
 C:Superfamily: scorpion
 C:Keywords: neurotoxin

The number of records received by chance to have a score greater than or equal to the score of the results being printed, and is derived by analysis of the total score distribution.

SCIMBRETT

| | | | | | | |
|----|------|------|------|---|---------|----------------------|
| 1 | 86 | 26.5 | 66 | 2 | A29386 | neurotoxin III - S |
| 2 | 80.5 | 24.8 | 65 | 2 | A59222 | neurotoxin X - S |
| 3 | 79.5 | 24.5 | 66 | 2 | A5869 | crustacean-specific |
| 4 | 79 | 24.4 | 85 | 2 | S68906 | alpha-toxin Bot X |
| 5 | 78.5 | 24.2 | 84 | 1 | NTSR3A | neurotoxin III pre- |
| 6 | 77 | 23.9 | 65 | 1 | NTSR4L | neurotoxin IV - E |
| 7 | 76.5 | 23.6 | 61 | 2 | B34123 | detrox toxin insect- |
| 8 | 76 | 23.5 | 66 | 1 | NTSR4E | neurotoxin M14 - |
| 9 | 75.5 | 23.3 | 65 | 1 | NTSR1C | neurotoxin 1 - ba- |
| 10 | 75 | 23.1 | 64 | 2 | JC1321 | neurotoxin IV - S |
| 11 | 74.5 | 23.0 | 70 | 2 | A55824 | dirosomycin precu- |
| 12 | 74 | 22.8 | 59 | 2 | C23727 | neurotoxin V-5 |
| 13 | 73 | 22.5 | 64 | 1 | T05RL | neurotoxin V - E |
| 14 | 71 | 21.9 | 1111 | | T269772 | humic/herical pro- |

RESULT 2
AS9222
neurotoxin X - Scorpion (*Leiurus quinquestratus*)
C. Scorp. *Leiurus minniestratus* hebraeus

C Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 19-Apr-2002

C Accession: A59222

R: Escudero, G.; Nakajima, T.

K: Description: A procedure for the rapid purification of non commercial and new scorpion

A: Reference number: A59222

A: Status: Preliminary

A: Molecule type: protein

A: Residues: 1-65 <BCU>

C: Superfamily: scorpion neurotoxin

C: Keywords: amidated carboxyl end; neurotoxin; venom

F:13 64 17 37 23 47 27 49/Disulfide bonds: #status Predicted

F:65/Modified site: amidated carboxyl end Arg; #status Predicted

Alignment Scores:

Pred No.: 3 2/7

Score: 80.50

Percent Similarity: 57.14

Best Local Similarity: 40.48

Query Match: 24.85%

DB: JS-09-673-274B-2 (1-169) x A59222 (1-65)

Length: 65

Matches: 17

Conservative: 7

Mismatches: 9

Indels: 3

Gaps: 4

Length: 11-169

Matches: 11

Conservative: 11

Mismatches: 11

Indels: 11

Gaps: 11

Length: 1-169

Matches: 11

Conservative: 11

Mismatches: 11

Indels: 11

Gaps: 11

Length: 1-85 <BCU>

Matches: 11

Conservative: 11

Mismatches: 11

Indels: 11

Gaps: 11

Length: 1-85

Matches: 11

Conservative: 11

Mismatches: 11

Indels: 11

Gaps: 11

Length: 1-85

Matches: 11

Conservative: 11

Mismatches: 11

Indels: 11

Gaps: 11

Length: 1-85

Matches: 11

Conservative: 11

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Length: 1-85

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Length: 1-85

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Mismatches: 11

Indels: 11

Gaps: 11

Length: 1-85

Matches: 11

Conservative: 11

Mismatches: 11

Indels: 11

Gaps: 11

Length: 1-85

Matches: 11

Conservative: 11

Mismatches: 11

Indels: 11

Gaps: 11

Length: 1-85

Matches:

RESULTS

RESULT 6

A:Reference number: A01749
A:Accession: A01749
A:Molecule type: Protein
A:Residues: 1-65
C:Species: Leirus quinquestriatus (Egyptian scorpion)
C:Accession: A01749
C:Title: Primary structure of toxin IV of Leirus quinquestriatus.
C:Keywords: blocked carboxyl end; neurotoxin; sodium channel inhibitor; venom
F:65/Modified site: blocked carboxyl end (Arg); (probably amidated) #status experimental

Alignment Scores:

| Pred. No.: | Score: | Length: | Matches: | Percent Similarity: | Conservative: | Best Local Similarity: | Mismatches: | Indels: | Gaps: |
|------------|--------|---------|----------|---------------------|---------------|------------------------|-------------|---------|-------|
| NTSR4L | 0.496 | 65 | 77/50 | 57.14% | 16 | 38.10% | 9 | 23.92% | 1 |

US-09-673-274B-2 (1-169) x NTSR4L (1-65)

Qy 16 TCCCTCGTGTGGCTGAACTACACTTCCGATTGAAAGGTGAGTCAGAGGG 75
Db 30 AsnCysValTyrrhCysVal-----ProProCysAspGlyLeuCysLysAsn 46

Qy 76 GGTACAAAGGTGGTCATCGCCTTC----GTTAACCTGAAGTCGGTGC 126
Db 47 GlyAlaLysSerGlySerCysGlyPheLeuIleProSerGlyLeuAlaCysTrpCys 65

RESULTS

RESULT 7

A:Reference number: B34123
A:Accession: B34123
A:Molecule type: protein
A:Residues: 1-61
C:Species: Leirus quinquestriatus (Egyptian scorpion)
C:Accession: B34123
C:Title: On the chemistry and action of the depressant insect toxins from the venom of Leiurus quinquestriatus
C:Keywords: neurotoxin; venom

Alignment Scores:

| Pred. No.: | Score: | Length: | Matches: | Percent Similarity: | Conservative: | Best Local Similarity: | Mismatches: | Indels: | Gaps: |
|------------|--------|---------|----------|---------------------|---------------|------------------------|-------------|---------|-------|
| NTSR4E | 0.496 | 65 | 77/50 | 57.14% | 16 | 38.10% | 9 | 23.92% | 1 |

US-09-673-274B-2 (1-169) x NTSR4E (1-65)

Qy 16 TCCCTCGTGTGGCTGAACTACACTTCCGATTGAAAGGTGAGTCAGAGGG 69
Db 12 AsnCysValTyrrhCysGlySerAsnSerTyr-----cysAspThrGlyCysThr 28

Qy 70 AGGGGGTTACAGGGTGTACTGCA----GGTCTCTCGCTAACGTGAACTGC 120
Db 29 LysAsnGlyAlaGluSerGlyTyrCysGinTrpLeuGlyLysTrpLeuGlyAsnAla--Cys 47

121 TGGTGC 126
Db 48 TrpCys 49

RESULTS

RESULT 8

A:Reference number: A94652
A:Accession: A94652
A:Molecule type: Protein
A:Residues: 1-66
C:Comment: The venom of this scorpion contains three major polypeptide neurotoxins: Mi4, Mi5, Mi6
C:Species: Mesobuthus eupeus (lesser Asian scorpion)
C:Accession: JTC020
R:Volkova, T.M.; Garcia, A.F.; Telezhinskaya, I.N.; Porapenko, N.A.; Grishin, E.V.
Bioorg. Khim. 11, 145-156, 1985
A:Title: Study of neurotoxins from the venom of central Asian scorpion Buthus eupeus.

Alignment Scores:

| Pred. No.: | Score: | Length: | Matches: | Percent Similarity: | Conservative: | Best Local Similarity: | Mismatches: | Indels: | Gaps: |
|------------|--------|---------|----------|---------------------|---------------|------------------------|-------------|---------|-------|
| NTSR4E | 0.496 | 66 | 76/50 | 58.62% | 16 | 44.63% | 8 | 23.46% | 1 |

US-09-673-274B-2 (1-169) x NTSR4E (1-66)

Qy 52 TGCACCGTGAGTCAGAGGGTTACAGG3GTGTCTGC-----GGTTC 102
Db 22 CysAspSerGlyCysLysAsnGlyAlaAspGlySerTyrCysGinTrpLeuGlyArg 44

Qy 103 TTGCTAACGTGAACTGCTGTCAG 129
Db 42 PheGlyAsnAsn---cystTrpCysLys 49

RESULTS

RESULT 9

A:Reference number: S08267
A:Accession: S08267
A:Molecule type: protein
A:Residues: 1-61
C:Species: Centruroides sculpturatus (bark scorpion)
C:Accession: A01752
R:Bobin, D.R.; Watt, D.D.; Goos, S.M.; Miejsnek, R.V.
Arch. Biochem. Biophys. 164, 694-706, 1974
R:Zlotkin, E.; Eitan, M.; Bindokas, V.P.; Adams, M.E.; Moyer, M.; Burkhardt, W.; Fowler,

A;Title: Amino acid sequences of neurotoxic protein variants from the venom of Centruroid
 A;Reference number: A90058; MUID:75163395; PMID:4463885
 A;Molecule type: protein
 A;Accession: AJ01752
 A;Residues: 1-65 <BAA>
 C;Species: scorpion neurotoxin
 C;Keywords: neurotoxic; venom
 F;12-64,ie 41-27-46,29-48/Disulfide bonds: #status predicted

Alignment Scores:
 Pred. No.: 0.861 Length: 65
 Score: 75.50 Matches: 44
 Percent Similarity: 51.35% Conservative: 5
 Best Local Similarity: 37.84% Wismatches: 5
 Query Match: 23.30% Indels: 3
 Gaps: 1

US-09-673-274B-2 (1 169) x NTSP-C (1-65)

Qy 19 TCGCTGGGGTGTGCT-GAACTACACTTCGATTGCAACGCTGAGTCAGAGGGGT 78
 3b 16 CysPheTrpLeuGlyLysAsnIluHsAsnThrCysGluCysAialysAshSlnGly 35

Qy 79 TACAAAGGGTGTCACTCGGTTCTCTGGCTAACGCTGCTGTCAG 129
 3b 36 GlySerTyGlyTyCysTrpCysTyAiaPheAla... CysteicGlu 49

JCL22 neurotoxin IV Sahara scorpion
 C;Species: Androctonus australis (Sahara scorpion)
 C;Date: 30-Sep-1993 #text_change 07-May-1999
 C;Accession: JC121
 A;Molecule type: protein
 A;Residues: 1-64 <MAN>
 C;Species: Y scorpion neurotoxin
 C;Keywords: neurotoxin

Alignment Scores:
 Pred. No.: C:99 Length: 64
 Score: 75.00 Matches: 45
 Percent Similarity: 51.22% Conservative: 5
 Best Local Similarity: 39.02% Wismatches: 10
 Query Match: 23.15% Indels: 4
 DB: 2 Gaps: 2

US-09-673-274B-2 (1 169) x JC121 (1-64);

Qy 52 TCCAAACGGTGTGACTGAGGAGGGTACAAAGGCTGCTACTGGGTTCTTC----- 1CS
 3b 20 CysAspPheLeuLysAsnIluAlaLysSerCysGlyPheLeuValPro 39

Qy 106 GTCACCTGAACACTGCTGTGCGGACATGAGAAGCTGGGGAGCGTCGACGGAT 165
 2b 40 SerCysLeuAlaCysTrpCysAsn-----AspLeuProGluAsnVa:ProIleLySAsp 57

JCL22 neurotoxin V - Egyptian scorpion
 C;Species: Leurus quinquespinatus (Egyptian scorpion)
 C;Date: 30-Apr-1979 #sequence_revision 13-Jul-1981 #text_change 15-Oct-1996

Alignment Scores:
 Pred. No.: C:99 Length: 59
 Score: 74.00 Matches: 46
 Percent Similarity: 60.53% Conservative: 7
 Best Local Similarity: 42.11% Wismatches: 7
 Query Match: 22.84% Indels: 8
 DB: 2 Gaps: 3

US-09-673-274B-2 (1 169) x C23727 (2 59)

Qy 16 TCCCTGCCTGTGGGTGACTACACTTCGGATGCAACGGTGTGAGTCAGAGGGGG 75
 14 SerCysVal-----AlaAsnAsnTrp-----CysAspAsnGlnCysAsnMetLys 28

Qy 76 GGTTACAAGGGTGTGCTGCGTTCTTCGCTAACGTGAACGTGCGTGGCGAG 129
 2b 29 LysAsnSerGlyIluHisCysTrpAla-----MetSerCysTrpCysGlu 43

RESULT 11

A55824 dromomycin precursor - fruit fly (Drosophila melanogaster)
 C;Species: Drosophila melanogaster
 C;Date: 23-Mar-1995 #sequence_revision 05-Apr-1995 #text_change 21-Jul-2000
 R;Fenbaum, P.; Bulet, P.; Michaud, M.; Lagautier, L.; Michaut, C.; Hotteman

C;Accession: A01741
R;Kopeyan, C.; Martinez, G.; Rochat, H.

FEBS Lett. 89, 54-58, 1978

A;Title: Amino acid sequence of neurotoxin V from the scorpion *Leiurus quinquestriatus*

A;Note: L.-Q. Quinquestriatus

A;Molecule type: protein

A;Residues: 1-64 <P>

C;Superfamily: scorpion neurotoxin

C;Keywords: blocked carboxyl end; neurotoxin; venom

P;12-63,16-36,22-26,48-Disulfide bonds: #status predicted

P;64/Modified site: blocked carboxyl end (Asn) (probably amidated) #status experimental

Alignment Scores:

| Pred. No.: | Score: | Percent Similarity: | Best Local Similarity: | Query Match: | DB: |
|------------|-------------|---------------------|------------------------|--------------|-----|
| 1.72 | 73.00 | 60.71* | 42.53* | 1 | DB: |
| Length: 64 | Matches: 12 | Conservative: 5 | Mismatches: 7 | Gaps: 2 | |
| | | | | | |

US-09-673-274B-2 (1-169) × NTSLRSL (1-64)

Qy 52 TGCACAGGTGAGTGAAGAGGGTTAACAGGCTGGTCAACTGC-----GGTCC 102
Db 22 Cy₃AsnAspGluCysLysLysGlyGluSerGlyTyrCysGlnTrpA₁aserPro 41

Qy 103 TTGGCTAACCTGAAGTGTGTC 126

Db 42 TyrglyAsnAla--cystrpCys 48

RESULT 14

Submitted to the EMBL Data Library, October 1998

A;Reference number: 220233

C;Species: *Caenorhabditis elegans*

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Accession: T26972

R;Harris, B.

Submitted to the EMBL Data Library, October 1998

A;Reference number: 220233

C;Species: *Caenorhabditis elegans*

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Accession: T26972

A;Residues: 1-111 <WIL>

A;Cross-references: EMBL:AL032657; PIDN:CAA21739.1; CESP:Y47H9C.4

A;Experimental source: clone Y47H9C

C;Genetics:

A;Gene: CESP:Y47H9C.4

A;Map position: 1

A;Introns: 50/2; 84/2; 150/1; 238/3; 342/3; 797/1; 851/1; 947/2; 1017/1; 1C83/1

C;Superfamily: unassigned ankyrin repeat proteins; ankyrin; repeat homology; EGF homology

Alignment Scores:

| Pred. No.: | Score: | Percent Similarity: | Best Local Similarity: | Query Match: | DB: |
|--------------|-------------|---------------------|------------------------|--------------|-----|
| 2.19 | 71.00 | 38.60* | 31.58* | 2 | DB: |
| Length: 1111 | Matches: 18 | Conservative: 4 | Mismatches: 17 | Indels: 18 | |
| | | | | | |

US-09-673-274B-2 (1-169) × T26972 (1-111)

Qy 49 GATGCC-----AAACGGTGAGTGGCAAGGAGGGGTAC 81
Db 293 AspCysLeuAsnAsnGlnAsnCysAspSerSerGlyGluC₃lysCysIleGlyTrp 312

Qy 82 AAAGGGTGTCACTGC-----GGTCCCTCGCTAACCTGAACTGCTG 114

Db 313 ThrglyLysIleCysAspIleGlyCysSerArgGlyArgGlyLeuGlnCysLysGln 332

Qy 115 AACGTCTGGTGGAGACTTGAGAGCTGGCCAGGGCAACGTGTGACGGAT 165

C;Accession: A01741
R;Kopeyan, C.; Martinez, G.; Rochat, H.

FEBS Lett. 89, 54-58, 1978

A;Title: Amino acid sequence of neurotoxin V from the scorpion *Leiurus quinquestriatus*

A;Note: L.-Q. Quinquestriatus

A;Molecule type: protein

A;Residues: 1-64 <P>

C;Superfamily: scorpion neurotoxin

C;Keywords: blocked carboxyl end; neurotoxin; venom

P;12-63,16-36,22-26,48-Disulfide bonds: #status predicted

P;64/Modified site: blocked carboxyl end (Asn) (probably amidated) #status experimental

Alignment Scores:

| Pred. No.: | Score: | Percent Similarity: | Best Local Similarity: | Query Match: | DB: |
|------------|-------------|---------------------|------------------------|--------------|-----|
| 1.72 | 73.00 | 60.71* | 42.53* | 1 | DB: |
| Length: 64 | Matches: 12 | Conservative: 5 | Mismatches: 7 | Gaps: 2 | |
| | | | | | |

US-09-673-274B-2 (1-169) × NTSLRSL (1-64)

Qy 52 TGCACAGGTGAGTGAAGAGGGTTAACAGGCTGGTCAACTGC-----GGTCC 102

Db 22 Cy₃AsnAspGluCysLysLysGlyGluSerGlyTyrCysGlnTrpA₁aserPro 41

Qy 103 TTGGCTAACCTGAAGTGTGTC 126

Db 42 TyrglyAsnAla--cystrpCys 48

RESULT 15

NTSR3C

C;Species: *Centruroides sculpturatus* (bark scorpion)

C;Date: 15-Oct-1982 #sequence revision 15-Oct-1982 #text_change 23-Aug-1986

C;Accession: A90058; MUID: A94470; ACI:754

R;Babin, D.R.; Watt, D.D.; Goos, S.M.; Mlejnek, R.V.

Arch. Biochem. Biophys. 164, 694-706, 1974

A;Title: Amino acid sequences of neurotoxic protein variants from the venom of Centruroides

A;Reference number: A90058

A;Molecule type: protein

A;Residues: 1-24, 'NTC', 28 63, 'CS' <SAB>

R;Brown, A.; Mo, J.; Fontecilla-Camps, J.C., et al., Toxicon 20, 17, 1982

unpublished results, cited by Fontecilla-Camps, J.C., et al.

A;Reference number: A94470

A;Accession: A94470

A;Molecule type: protein

A;Residues: 1-65 <RHO>

R;Fontecilla-Camps, J.C.; Almassy, R.J.; Sudath, F.L.; Bugg, C.F.

Toxicon 20, 1-7, 1982

A;Title: The three-dimensional structure of scorpion neurotoxins

A;Reference number: A94311; MUID: 8220025; PMID: 780025

A;Contents: annotation: X-ray crystallography, 1.8 angrstroms; disulfide bonds

C;Supertamily: scorpion neurotoxin

C;Keywords: neurotoxin; venom

F;12-65,16-41,25-46,29-49/distifide bonds: #status experimental

Alignment Scores:

| Pred. No.: | Score: | Percent Similarity: | Best Local Similarity: | Query Match: | DB: |
|------------|-------------|---------------------|------------------------|--------------|-----|
| 3.42 | 70.50 | 51.22* | 36.59* | 1 | DB: |
| Length: 65 | Matches: 15 | Conservative: 6 | Mismatches: 13 | Indels: 7 | |
| | | | | | |

US-09-673-274B-2 (1-169) × NTSLRSL (1-64)

Qy 19 TGCCTGCTGGGCTGCTGTAAACCTAC-----ACTTCGGATTCAACGGTGAAGTGC 72

Db 12 CysLysTyrGlyCysCysLysLysGlyGluSerGlyAspThrGlyCysAspLysAsn 31

D3: 1

Gaps: 3

US-09-673-274B-2 (1-169) × NTSLRSL (1-64)

Qy 19 TGCCTGCTGGGCTGCTGTAAACCTAC-----ACTTCGGATTCAACGGTGAAGTGC 72

Db 12 CysLysTyrGlyCysCysLysLysGlyGluSerGlyAspThrGlyCysAspLysAsn 31

D3: 1

Gaps: 3

US-09-673-274B-2 (1-169) × NTSLRSL (1-64)

Qy 73 AGGGTACAAGGGT-----GGTCACTGCGTTCCTTCGGTAACCTGAACTGCTG 126

Db 32 LysAsnGlnGlyGlySerTyrGlyTyrCysTyrAlaPheAla-----CysTyrGly 48

Qy 127 GAG 129

Db 49 Glu 49

Search completed: October 16, 2003, 17:11:58

Job time : 23.771 secs